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GenCore version 5.1.3
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- protein search, using sw model OM protein December 30, 2002, 20:40:02; Search time 51 Seconds Run on:

(without alignments)
772.845 Million cell updates/sec

US-09-699-652A-14

Perfect score: Title:

1 MAMAGHAPGGALPLILLVVS.....DDVYVDLIRFLRENGWHNSY Sequence:

410

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\* Database :

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	.1055	48.1	344		E84526	probable lysosom
2	557.5	ď.	403		T33198	ical
m	553	5	397		JC4017	triacylqlycerol
4	549	5	405		T22675	hypothetical pro
2	546	4.	398		S07145	triacylalycerol
ø	539.5	4.	395		LIRT	triacylqlycerol
7	523	ω.	405		H88930	protein RilG11.1
œ	515.5	ω.	399		S41408	lysosomal acid l
σ	513	ω.	399		G01416	lysosomal acid l
10	500.5	22.8	426	7	T20480	hypothetical pro
11	474	ä	411		T22290	
12	466.5	ä	411		G89074	protein K04A8.5
13	416.5	φ.	559		JT0949	egg-specific pro
14	392.5	۲.	1585		T31611	hypothetical pro
15	356	ė.	443		T39540	triglyceride lip
16	345.5	ď.	467		T41053	triglyceride lip
17	309	4.	460		T39443	probable triglyc
18	293.5	m.	548		837969	
19	259.5	Ξ.	413		T43170	
20	254	;	538		S64842	
21	237	ö	573		S64754	probable membran
22	212	•	431		D86318	protein F15H18.6
23	170.5		509		G96766	protein lipase F
24	165		336		F83425	
25	147		460		G96764	unknown protein
56	121.5	•	456		E69391	hypothetical pro
27	110.5	•	666		B70501	hypothetical pro
28	108.5	•	1002		87	long
29	107.5	6.4	841		A90669	probable enzyme

ore of the control of

9 841 2 D85519 1.9 841 2 C64755 1.6 1216 2 F88473 1.5 323 2 F88473 1.5 323 2 F88473 1.4 465 1 JC1318 1.4 467 1 LIDG 1.3 1648 2 S71654 1.3 1648 2 F81654 1.3 2100 2 T03223 1.3 2100 2 T03223 1.3 2100 2 A47563 1.3 2100 2 A47563 1.3 2100 2 A47563 1.3 2100 2 A47563	
	A97648
	7
<u> એએઌ૽ઌ૽ઌ૽૱૱૱</u> ઌ૽ઌઌઌઌઌ	269
<b>4 4 4 4 4 4 4 4 4 4 4 5</b>	4.3
1007.5 1007.5 1009.9 997.5 95.5 95.5 95.5 95.5	94
0 11 12 13 13 13 13 13 14 14 14 14 15 15 16 16 16 16 16 16 16 16 16 16 16 16 16	

## ALIGNMENTS

526 .	pecies: Arabidopsis thaliana (mouse-ear cress)	ccession: E84526	Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.
bable lysosomal acid libase (imported) - Arabidoosis thallana	ate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	in, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; F	S. D.; Nierman, W.C.; White, O.: Eisen, J.A.; Salzberg, S.L.: Fraser, C.M
omal acid libase (imported) - Ar	abidopsis thaliana (mouse-ear cre-	584526	Woffat, K.S.; Cronin, L.A.; Shen,
	b-2001 #sequence_revision 02-Feb-	11, S.; Rounsley, S.D.; Shea, T.P	rman, W.C.: White, O.: Fisen, J.A.

Town, C.D.; Fujii, C.Y E.; Umayam, L.; Tallon, .; Fraser, C.M.; Venter A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: A84420; MUID:20083487; PMID:10617197 A:Accession: E84526 Nature 402, 761-768, 1999 Probi C;Sp C;Da C;Ac C;Ac R;Lil M;

A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-344 <STO>
A; Cross-references: GB:AE002093; NID:g4585908; PIDN:AAD25569.1; GSPDB:GN00139
C; Genetics:
A; Gene: At2g15230

A; Map position:

~ Gaps 52; Length 344; Indels ; Score 1055; DB 2; ; Pred. No. 4.2e-82; 42; Mismatches 71; 48.1%; 54.5%; Query Match Best Local Similarity 54.5% Matches 198; Conservative

40 GSGSGCLCDQLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTGPPVFLQHGLFQ 99 ô qq

100 GGDTWFINSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEY 159 δ Q

160 DLLAMLGYVYTVTQSKILYVGHSQGTIMGLAALTMPEIVKMISSAALLCPISYLDHVSAS 219 ò q

220 FVLRAVAMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVDCNNLLSAITGENCCFNT 279 ò

204 LVERMVFMHLDQ----g

-:IEYYLDYEPHPSSVKNIRHLFQMIRKGTFAQYDYGYFKNLRTYGLSKPPEFILSHIPA 273 280 SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSIPE 339 216 δ Q

340 SLPIWMGYGGLDALADVTDVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLIR 399 274 ŏ g

FLR 402 400 δλ

336 FFR 334

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Query Match
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hypothetical protein 2K6.7 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: T3198
R; Mu, X.
submitted to the EMBL Data Library, May 1998
A; Description: The sequence of C. elegans cosmid ZK6.
A; Reference number: Z21301
A; Accession: T3198
A; Accession: T3198
A; Accession: T3198
A; Accession: T3198
A; Residues: 1-403 < WUX>
A; Cross-references: EMBL: AF067942; PIDN: AAC17694.1; GSPDB: GN00023; CESP: ZK6.7
A; Experimental source: strain Bristol N2; clone ZK6
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triacylglycerol lipase (EC 3.1.1.3) PGE precursor - bovine
N.Alternate mames: pregastric esterase
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC4017; S64678
R;Timmermans, M Y.J.; Teuchy, H.; Kupers, L.P.M.
Gene 147, 259-262, 1994
A;Title: The cDNA sequence encoding bovine pregastric esterase.
A;Title: The cDNA sequence encoding bovine pregastric esterase.
A;Reference number: JC4017; MUID:95011625; PMID:7926811
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-397 < TIM>A;Residues: 1-397 < TIM>A;Cross-references: GB:L26319; NID:9600756; PIDN:AAA57037.1; PID:9600757
A;Experimental source: tongue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 LRAVAMHLDQMLVTMGIHQL----NFRSDMGVQIVDSLCDGEHVD----CNNLLSAITG-EN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PDYLLTRLNPAIVAQNNHLPDYNHL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 YVYTVT-QSKILYVGHSQGTIMGLAALTMPE--IVKMISSAALLCPISYLDHVSA--SFV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 ANYFSLEFDGWFDIFGAGEFLPNNWAMKLAAK---DICGGLKVEADLCDNVLFLIAGPES 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 CCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSIPESLPIWMGYGGLDALADVTDVORTIRELGSTPELL------YIGDYGHI 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 QIIERWGYPAMIYTVATDDGYILEMHRIPFGKTNVTWPNGKRPVVFMQHGLLCASSDWVV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 557.5; DB 2
Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Mismatches
                                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:ZK6.7
A;Map position: 5
A;Introns: 29/3; 63/1; 219/3; 319/3; 365/3
C;Superfamily: triacylglycerol lipase, lingual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 TAI-KGTKIYLYWSDADWLADTPDV---
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Matches 124; Conservative
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R;Timmermans, M.Y.J.; Reekmans, G.; Teuchy, H.J.H.; Kupers, L.P.M.
Biochem. J. 314, 931-936, 1996
A;Title: Inhibition studies on calf pregastric esterase: the enzyme has no functional A;Reference number: $64678; MUD:96177869; PMID:8615791
A;Recension: $64678
A;Molecule type: protein
A;Residues: 24-40;248-253 <TIW>
C;Comment: Pregastric esterase is a major fat-digesting enzyme.
C;Genetics:
A;Genetics:
A;Genetics
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R; Percy, C.; Lloyd, C.
submitted to the EMBL Data Library, September 1996
A; Reference number: 219598
A; Accession: T22675
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-405
A; Cross-references: EMBL: Z79696; pIDN: CAB01973.1; GSPDB: GN00023; CESP: F54F3.3
A; Experimental source: clone F54F3
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C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : |||:||| |:||| |:||| |: || |: || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :| || :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGHIDFVMSVKAKD 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 AMHL------DQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 405;
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Best Local Similarity 34.9%; Pred. No. 3.2e-39;
Matches 130; Conservative 67; Mismatches 146;
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No. 7.1e-39;
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A;Introns: 31/3; 65/1; 274/3; 366/3
C;Superfamily: triacylglycerol lipase, lingual
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383 EVYNEIVSLMAED 395
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A. Molecule type: mRNA
A. Residues: 1-395 <- DOC>
A. Residues: 1-395 <- Doc-
A. Residues: 1-395 <- Doc-
A. Residues: 1-395 <- Doc-
A. Residues: 1-300 <- Doc
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-59p-1987 #sequence_revision 30-Sep-1987 #text_change 11-Jun-1999
C;Accession: A.31045
R;Docherty, A.J.P.; Bodmer, M.W.; Angal, S.; Verger, R.; Riviere, C.; Lowe, P.A.; Lyo
Nucleic Acids Res. 13, 1891-1903, 1985
A;Title: Molecular cloning and nucleotide sequence of rat lingual lipase cDNA.
A;Reference number: A23045; MUID:85215587; PMID:3839077
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                                                        YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLR 223
                                                                                                                                                                                                                                                                                                                                                                                                            LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR 323
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                                                                                                           FLGTEV----CSREVLDLLCSNTLFIFCGFDKKNLNVSRFDVYLGHNPAGTSVQDFLHWA
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Pred. No. 4.4e-38;
                                                                                                                                                                                                                                                                                                                    216 FVPQSLFKFIFGDKIFYPHNFFDQFLAT----
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                                                                                                                                                                                                                                                                                                                        221
                                                                                    OLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 LRAVAMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-ENCCF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --YIGDYGHIDFVM 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                     NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                  YVYTVT-QSKILYVGHSQGTIMGLAALTMPEI--VKMISSAALLCPISYLDHVSAS--FV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADYFSLEFDGWFDVFGSGEFLPNNWIMKLVSESVCAGLKVEAGVCDDVMFLIAGPESNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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33.9%; Pred. No. 1.3e-38;
.ive 70; Mismatches 132; Indels
    Indels
    Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PESLPIWMGYGGLDALADVTDVQRTIRELGSTPELL-
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 GLRAPKDIYEPIIDIVRND 400
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Conservative
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Matches 130; Conservative
121;
    Matches
                                                                                                                                                                            33
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A; Cross-references: BMBL:X76488; NID:g434305; PIDN:CAA54026.1; PID:g434306
R; Anderson, R.A.; Sando, G.N.
J; Biol. Chem. 266, 22479-22484, 1991
A; Title: Cloning and expression of cDNA encoding human lysosomal acid lipase/choleste A; Reference number: A39315; MUID:92042192; PMID:1718995
A; Retence number: A39315; MUID:92042192; PMID:1718995
A; Retence number: A39315
A; Retence number: A39315
A; Residues: 1-15, 'P', 17-399 < AND>
A; Residues: 1-15, 'P', 17-399 < AND>
A; Residues: 1-15, 'P', 17-399 < AND>
A; Cross-references: GB:M74775; NID:g187151; PIDN:AAA59519.1; PID:g187152
R; Du, H.; Gregory, G.A.
Submitted to the EMBL Data Library, April 1994
A; Description: Structural conservation of putative functional motifs between mouse an A; Reference number: S47187
A; Accession: S47187
A; Residues: preliminary
A; Accession: S47187
A; Residues: 1-22, 'R', 24-399 < DUH>
A; Residues: L-22, 'R', 24-399 < DUH>
A; Residues: L-22, 'R', 24-399 < DUH>
A; Cross-references: EMBL:Z31690; NID:g506430; PIDN:CAA83495.1; PID:g506431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GEHVDCNNLLSAITGENCCF-----NTSRIDYYLEYEPHPSSTKNL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 PQSAFLKWLGTHVCTHVILKELCG-NLCFLLCGFNERNLNMSRVDVYTTHSPAGTSVQNM 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 PVFLQHGLFQGGDTWFINSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFW 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 VVFLQHGLLADSSNWVTNLANSSLGFILADAGFDVWMGNSRGNTWSRKHKTLSVSQDEFW 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHLFQMIRKGTFAKYDYGLLG-NLRRYGHLRPPAFDLSSIPESLPIWMGYGGLDALADVT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DWSWQELAEYDLLAMLGYVYTVT-QSKILYVGHSQGTIMGLAALT-MPEIVKMISSAALL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GPVA----SVAFCTSPMAKLGRLPDHL-------IKDLFGDKEFL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 GSGGL------CDQLLLPLGYPCTEHNVETKDGFLLSLQHIPHG-KNKAADSTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GSGGKLTAVDPETNMNVSEIISYWGFPSEEYLVETEDGYILCLNRIPHGRKNHSDKGPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 CPISYLDHVSASFVLRAVAM-----HLDQMLVTMGIHQLNFRSDMGVQIVDSLCD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLIRFLRE 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:120153; OMIM:278000
A; Map position: 10q24-10q25
C; Superfamily: tilacylylycerol lipase, lingual
C; Keywords: carboxylic ester hydrolase; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April 1994
A;Reference number: G06919
A;Accession: G01416
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 23.5%; Score 515.5; DB Best Local Similarity 32.3%; Pred. No. 5e-36; Matches 131; Conservative 59; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lysosomal acid lipase - human
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C;Date: 21-Dec-1996 #sequence
                       1-399 <AME>
Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: LIPA
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                                                                                                                                                                           proceson R1G11.14 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C; Accession: H88330
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans; a platform for investigating biolog
A; Reference number: A75000: MUID: 99069613; PMID: 9819196
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A; Note: spublished errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A; Accession: H89330
A; Retaicus: prellininary
A; Molecule type: DNA
A; Residues: 1-405 <270A
A; Cross-references: GB:Chr_V; PIDN:AAC69088.1; PID:g2384863; GSPDB:GN00023; CESP:R11G11.
A; Note: Similar to lipase; R11G11.14
C; Genetics:
A; Gene: R11G11.14
A; Map posttion: 5
C; Superfamily: triacylglycerol lipase, lingual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C; Accession: 841408; A39315; S47187
C; Accession: 841408; A39315; S47187
Eur. J. Biochem. 219, 905-914, 1994
A; Title: Purification, characterization and molecular cloning of human hepatic lysosomal A; Reference number: 841408; MUID:94155897; PMID:8112342
A; Accession: 841408
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AHYFSLEFDGWFDVFGAGEFLPNNWAMKLAAK---DICGGLKIESDLCDNVCFLIAGPES 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYG-HLRPPAFD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 DOWNSTRVPVYASHDPAGTATONIVHWIOMVRHGGVPAYDWGSKENKKNVNFQANPPEYD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELL----YIGDYGHIDFVMSVKA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTAI-KGTQIYLYWSDADWLADKTDITNYLL-TRLNPAIIAQNNYFTDYNHFDFVFGLRA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 YVYTVT-QSKILYVGHSQGTIMGLAALTMPE--IVKMISSAALLCPISYLDHVSA--SFV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 KVLEVTGQESLYYMGHSQGTLTMFSHLSKDDGIFAKKIKKFFALAPVGSVKDIKGFLSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRAVAMHLDQMLVTMGIHQL---NFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                               353 LLPKLSN---LLFHKEILAYNHLDFIWAMDAPQEVYNEMISMMAED 395
TIRELGSTPELLY --- IGDYGHIDFVMSVKAKDDVYVDLIRFLREN 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.8%; Score 523; DB 2; 32.2%; Pred. No. 1.2e-36; iive 67; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 32.2
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNDIYLPIV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDDVYVDLI 398
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157 KQEFLYYLGHSQGTMIMFSRLAENPEFAKKIRHFHALAPVATVSHIGGLFGLFGTKFLTY 216
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                                     229
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cat-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20480
R;Hembry, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: 219280
A;Accession: T20480
A;Accession: T20480
A;Reference number: Lype: DNA
A;Reference: DNA
A;Residues: 1-426 cWIL>
A;Residues: 1-426 cWIL>
A;Cross-references: EMBL;281055; PIDN:CAB02896.1; GSPDB:GN00022; CESP:F01G10.7
A;Experimental source: clone F01G10
C;Genetics:
A;Gene: CESP:F01G10.7
                                                                                                                     11;
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                                                                                                                                                  GYPCTEHNVETKDGFLLSLQHIPHG-KNKAADSTGPPVFLQHGLFQGGDTWFINSAEQSL 113
                                                                                                                                                                 GYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGYVYTVT- 172
                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                  219
                                                                                                                                                                                                                                                                                                                                               --HLDQMLVTMGIHQLNFRSDMGVQIVDSLCD------GEHVDCNNLLSAITG 272
                                                                                                                                                                                                                                                                                                                                                                                                              ENCCF-----NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLG-NL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHYNOSYPPTYNVKDMLVPTAVWS--GGHDWLADVYDVNILLTQITNLVFHESIPEWEHL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYPCTEHNVETKDGFLLSLQHIPHGKNKAAD -- STGPPVFLQHGLFQGGDTWFINSAEQS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGYVYTVT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSKIL-YVGHSQGTIMGLAALT-MPEIVKMISSAALLCPISYLDHVSASFVLRAVAM--H 228
                    PIDN: AAB60328.1; PID: 9505053
                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                QSKILYVGHSQGTIMGLAALT-MPEIVKMISSAALLCPISYLDHVSASFVLRAVAM----
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                                                                                                                                                                                                                                                                                                                                                                     220 PDHL-------INDLEGDKEFLPQSAFLKWLGTHVCTHVILKELCG
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                                                                                                                   62;
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                                                                                   Length 399;
                                                                                 Query Match 23.4%; Score 513; DB 2; Length 39 Best Local Similarity 33.2%; Pred. No. 8.2e-36; Matches 127; Conservative 56; Mismatches 137; Indels
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A; Residues: 1-399 <DUX>
A; Cross-references: BMBL:U08464; NID:9505052; F
C. Superfamily: triacylglycerol lipase, lingual
C; Keywords: 91ycoprotein
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A;Introns: 29/3; 64/1; 186/3; 347/2
C;Superfamily: triacylglycerol lipase, lingual
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Matches 117; Conservative
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Best Local S
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A;Cross-references: EMBL:Z70780; PIDN:CAA94824.1; GSPDB:GN00023; CESP:F46B6.8
A;Experimental source: clone F46B6
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C.Species: Caenorbadditis elegans
C.Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C.Accession: T22290
S.McMurray, A.
Submitted to the EMBL Data Library, April 1996
A.Reference number: 219542
A.Recession: T22290
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                    49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 YVYTVT-QSKILYVGHSQGTIM---GLAALTMPEIVKMISSAALLCPISYLDHVSA--SF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 FAHKFSPEFDGWYELFGSKDFLPDNWITKMAAKDICGASEKEAELCDNELFLIGGPESDQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 FNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 IPESLPIWMGYGGLDALADVTDVQR-TIRELGST--PELLYIGDYGHIDFVMSVKAKDDV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITGENCCFNTSRIDYYL
                                                          217 AEILLGRLPYSPLSIPRTV-QKMISYMCSRFFMQNICTLDIGFIDGNEKMFNQSRVGVYL
                                                                                                               EYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSIPESLPIWMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 VLRAVAMHLDOMLVTMGIHQL-..NFRSDMGVQIVDSLCDGEHVDCNNLLSAITG-ENCC
                                                                                                                                                                                                                                                                          334 WSRDDILADIQDIRDSILSKMNKTIAGSLELPH---YSHMDFVFGTHAAFDLY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                        347 YGGLDALADVTDVQRTI-----RELGSTPELLYIGDYGHIDFVMSVKAKDDVY 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 411;
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31.7%; Pred. No. 1.8e-32;
ive 64; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F46B6.8 - Caenorhabditis elegans
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A;Introns: 35/3; 69/1; 104/1; 226/3
C;Superfamily: triacylglycerol lipase, lingual
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A; Residues: 1-411 <WIL>
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YDKAIK 401
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DEVMSVKAKDDVYVDLIRFLREN 404
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Best Local
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C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: G89074
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:990605613; PMID:981916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <STO>
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 LSSIPESLPIWMGYGGLDALADVTDVQRTI-RELGS--TPELLYIGDYGHIDFVMSVKAK 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 FINSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSV-HDKLFWDWSWQELAEYDLLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L--RAVAMHLDQMLVTMGIHQLNFRSDMGVQIVDSLC---DGEHVDCNNLLSAITG---E 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGK----NKAADSTGPPVFLQHGLFQGGDTW 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 FLGRHFGKDYEEYVKKHGSDELFGSSLLFKKIVKYTCGLFDTLEEFCSDITLLFIGTANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.3%; Score 466.5; DB 2;
32.4%; Pred. No. 7.8e-32;
tive 62; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 5
C; Superfamily: triacylglycerol lipase, lingual
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Matches 118; Conservative
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JT0949
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A;Map position: 19
C;Keywords: egg yolk; homotrimer
133-133-133/Cleavage site: Lys-Asn (egg 30.5K cysteine proteinase) #status experimental
F;228-229/Cleavage site: Arg-Asp (egg 30.5K cysteine proteinase) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1585 <WIL>
A;Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050.1; CESP:Y50E8A.9
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C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 ASEPPSYDLSKV--SAPVNL-YHSHDAMLAHPKDVEKLQENLPNVKQSFEVPEQQHFTDL 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKL--FWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                                                                                                                                                                                        225 VA------MHLDQM---LVTMGIHQLN-----FRSDMGVQIVDSLCDGEHVDCNNLL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTGPPVFLQHGLFQGGDTWFINS 108
                                                                                                                                                                                                                                                                                                                            194 ELLKKHQYPVEEHTVATDDGYHLTVLRIPPTHQTRDDKKKPVALLMHGLLGSADDWLLMG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVYTVT-QSKILYVGHSQGTIMGLAALT-MPEIVKMISSAALLCPISYLDHVSASFVLRA 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 SAITGENCCFNTSR--IDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 HLRPPAFDLSSIPESLPIWMGYGGLDA-LADVTDVQRTIRELGSTPELLYIGDYGH---I
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                                                                                                                                             Length 559
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A;Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2
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ilarity 27.5%; Pred. No. 9.6e-25;
Conservative 68; Mismatches 188;
                                                                                                                                                DB 2;
                                                                                                                                                                                                          64; Mismatches 152;
                                                                                                                                             Query Match 19.0%; Score 416.5; DB 2
Best Local Similarity 31.9%; Pred. No. 2.2e-27;
Matches 122; Conservative 64; Mismatches 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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R)Steward, C.
Submitted to the EMBL Data Library, September 1999
A)Reference number: 221047
A)Accession: T31611
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RESULT 15
T39540
triglyceride lipase-cholesterol esterase - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Accession: T39540
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
Submitted to the EMBL Data Library, February 1998
A; Reference number: Z21862
A; Accession: T39540
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T39540
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Georetics:
A; Georetics:
A; Georetics:
A; Georetics:
A; Georetics:
A; Georetics:
A; C; Superfamily: triacylglycerol lipase, lingual
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                                                                                      169 VMFARLAEADVTWQSKIRVFFALGPTAGFMKPLMPFTLLEENYLQALIQFALDG---KFG 225
                                                                                                                                                                                IHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITGENCC--FNTSRIDYYLEYEPHPS 293
                                                                                                                                                                                                                                                   | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                 STKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSIPESLPIWMGYGGLDAL 353
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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                                   1 | 1: | 1 | 1 | 1 | 216 IPHFLFKIIFGDKMFYP---HTF-LEQFLGVE----MCSRETLDVLCKNALFAITGVDNK 267
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36 QMISYWGYPSEMHKVITADGYILQVYRIPHGKNNANHLGQRPVVFLQHGLLGSATNWISN 95
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Bernbaeck S., Blaeckberg L.;
"Human gastric lipase. The N-terminal tetrapeptide is essential for
lipid binding and lipase activity.";
Eur. J. Biochem. 182:495-499(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of human gastric lipase and model of lysosomal acid lipase, two lipolytic enzymes of medical interest.";
J. Biol. Chem. 274:16995-17012(1999).
-i. CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol +
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                                                                                    X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE-99287897; PubMed-10358049;
Roussel A., Canaan S., Egloff M.P., Riviere M., Dupuis L., Verger Cambillau C.;
                        SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGY
                                                                                                                       AMHL-----DQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENC
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Catarrhini; Hominidae; Homo.
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric lipase) (GL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87299724; PubMed-3304425;
Bodmer M.W., Angal S., Yarranton G.T., Harris T.J.R., Lyons A.,
King D.J., Pieroni G., Riviere C., Verger R., Lowe P.A.;
"Molecular cloning of a human gastric lipase and expression of
                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                             PRT;
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Eukaryota, Merazoa, Chordata,
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_site.
InterPro; IPR000179; Ser_estrs_site.
InterPro; IPR00120; LipAsf_SER; 1.
InterPro; IPR05TFE; PS00120; Lipid degradation; Glycoprotein; Signal; Polymorphism;
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33.9%; Pred. No. 1.2e-39;
iive 70; Mismatches 132; Indels
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N-LINKED (GLCNAC...).
N-LINKED (GLCNAC...).
T.-> A (IN DESNP: 814628).
/FTId-VAR_011947.
Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "TIG=VAR_011947.
CD3EE1621C014F0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          TRIACYLGLYCEROL LIPASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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(Rel. 05, Last sequence update)
modified and this statement is not removed
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                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                      EMBL, X05997; CAA29413.1; -.
EMBL, X05997; CAA29414.1; ALT_INIT.
EMBL, A01046; CAA00125.1; -.
EMBL, A12714; CAA01053.1; -.
PIR; S04942; S04942.
PIR; S07145; S07145.
PDB; 1HG; 15-MAR-00.
Genew; HGNC: 6622; LIPF.
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LDFIWAMDAPQEVYNDIVSMISED 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 AA; 45237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 33.99
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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398
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                                                                                                                                                                                                                                       MIM; 601980;
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13-AUG-1987
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P04634;
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ACT_SITE
DISULFID
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ACT_SITE
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QMIRKGTFAKYDYGLLG-NLRRYGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQR 361
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                 303
                                                                                                                                                 LIPG_CANFA
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                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                          fatty acid anion.
-!- MISCELLANEOUS: LINGUAL LIPASE IS SECRETED BY THE SEROUS (VON EBNER'S) GLANDS AT THE BACK OF THE RAT TONGUE.
-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLQHIPHGKNKAAD-STGPPVFLQHGLFQGGDTWFINSAEQSLGYILADNGFDVWIGNVR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |||||| : | | ||||||| | 5 GVRIPHGRNNSENIGKRPVVYLQHGLIASATNWIANLPNNSLAFMLADAGYDVWLGNSR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 GTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGYVYTVT-QSKILYVGHSQGTIMGL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | || : : :| || :| :| :| || :| GNTWSRKNVYYSPDSVEFWAFSFDEMAKYDLPATINFIVQKTGQEKIHYVGHSQCTTIGF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 IAFSTNPTLAKKIKTFYALAPVATVKYTQSPLKKISFIPTFLFKLMFGKKMFLPHTYFDD 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                MEDLINE-85215587; PubMed-3839077; Docherty A.J.P., Bodmer M.W., Angal S., Verger R., Riviere C., Lowe P.A., Lyons A., Emtage J.S., Harris T.J.R.; "Molecular cloning and nucleotide sequence of rat lingual lipase
                                                                                                                                                                                   Nucleic Acids Res. 13:1891-1903(1985).
-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
15-JUN-2002 (Rel. 41, Last annotation update)
Triacylglycerol lipase, lingual precursor (EC 3.1.1.3) (Lingual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 395;
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CHARGE RELAY SYSTEM (BY S
CHARGE RELAY SYSTEM (BY S
CHARGE RELAY SYSTEM (BY S
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (PP
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E601854A923522EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE SER;
Hydrolase; Lipid degradation;
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PIR; A23045; LIRTT.
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371
254
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98
                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                           NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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ACT_SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatty acid anion.
-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
lipase.";
Eur. J. Biochem. 202:75-83(1991).
-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
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Y SIMILARITY).
Y SIMILARITY).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                        LIPG_CANFA STANDARD; PRT; 398 AA.
P80035; 002857;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triacylelycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carriere F., Moreau H., Raphel V., Laugier R., Benicourt C., Junien J.-L., Verger R., "Purification and biochemical characterization of dog gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Stomach;
Vaganay S., Joliff G., Bertaux O., Toselli E., Devignes M.D.,
Renicourt C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 398;
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                                                                                                  Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                   362 TIRELGSTPELLY---IGDYGHIDFVMSVKAKDDVYVDLIRFLREN 404
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CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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PIR: S19539; S19539.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000073; Lipase.
Pram: PF00561; abhydrolase; 1.
PROSTE: PS00120; LIPASE_SER: 1.
BYdrolase: Lipid degradation; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> T (IN REF. 2).
E04D62F7518E386C
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MEDLINE=92037652; PubMed=1935982;
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99 N
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327 N
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45130 MW;
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Best Local Similarity
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265
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                                                                                                                                     LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR 323
                                                                                                                                                                            QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                   Du H., Witte D.P., Grabowski G.A.;
"Tissue and cellular specific expression of murine lysosomal acid
lipase mRNA and protein.";
           107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG
                                                                                 167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA----
                                                                                                                         ---SFVLRAVAMH------LDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
                                                                                                                                                                                                        YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVIDVQRTIRELGSTPELLY - - - IGDYGH
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 196-212; 277-297 AND 305-315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson R.A., Sando G.N.; "Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesteryl ester hydrolase. Similarities to gastric and
                                                                                                                                                                                                                                                                                                                             P38571; Q16529; Q96EJO; O1-0CT-1994 (Rel. 30, Created) O1-0CT-1994 (Rel. 30, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lysosomal acid lipase/cholesteryl ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ameis D., Merkel M., Eckerskorn C., Greten H.; "purification, characterization and molecular cloning of human hepatic lysosomal acid lipase."; Eur. J. Biochem. 219:905-914(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     399 AA.
                                                                                                                                                                                                                                                                                                                                                                                             esterase) (Lipase A) (Cholesteryl esterase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lingual lipases.";
J. Biol. Chem. 266:22479-22484(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92042192; PubMed=1718995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94155897; PubMed=8112342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96363957; PubMed=8725147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nase mRNA and protein.";
Lipid Res. 37:937-949(1996).
                                                                                                                                                                                                                                               381-IDFVMSVKAKDDVYVDLIRFL 401
                                                                                                                                                                                                                                                                  373 LDFIWAMDAPOAVYNEIVSMM 393
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-Placenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                       LICH_HUMAN
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                                                                                                                                                                                                                          MEDLINE-98395576: PubMed-9653819;

A Ries S., Buechler C., Schindler G., Aslanidis C., Ameis D., Gasche C., Jung N., Schambach A., Fehringer P., Vanier M.T., Belli D.C., Grembach A., Fehringer P., Vanier M.T., Belli D.C., Jung N., Schamitz G.;

Tulpase cause cholesteryl ester storage disease in unrelated compound in the coordinesteryl ester storage disease in unrelated compound the telecotygous and hemizygous individuals.";

Hum. Mutat. 12:44-51(1998).

- !- FUNCTION: CRICIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTORMEDIATING THE EFFECT OF LID. (LOW DENSITY LIPOPROTEIN) UPTAKE ON SUPPRESSION OF HYDROXYMETHYLGLUTARRYL CAR REDUCTASE AND ACTIVATION OF ENDOCENOUS CELLULAR CHOLESTERYL ESTER FORMATION.

C. CATALYTIC ACTIVITY: A steryl ester + H(2)O = a sterol + a fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: DEFECTS IN LIPA ARE THE CAUSE OF THE SEVERE INFANTILE-
NOSET WOLMAN DISEASE (WD) AND THE MILDER LATE-ONSET CHOLESTERYL
ESTER STORAGE DISEASE (CESD).
SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE.
VARIANT CESD/WD PRO-200.
MEDLINE-94195814; PubMed-8146180;
Anderson R.A., Byrum R.S., Coates P.M., Sando G.N.;
"Mutations at the lysosomal acid cholesteryl ester hydrolase gene locus in Wolman disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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Hydrolase; Lipid degradation; Glycoprotein; Signal; Lysosome;
                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 91:2718-2722(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L; U04285; AAB60327.1; -. 104286; AAB60327.1; -. 104286; AAB60327.1; JOINED. L; U04288; AAB60327.1; JOINED. L; U04291; AAB60327.1; JOINED. L; U04291; AAB60327.1; JOINED. L; U04292; AAB60327.1; JOINED. L; U04293; AAB60327.1; JOINED. L; X76488; CAA54026.1; -.
                                                                                                                                                                                                              VARIANTS CESD ARG-129 AND PRO-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000073; Abhydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z31690; CAA83495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M74775; AAA59519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U08464; AAB60328.1; -. BC012287; AAH12287.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000734; Lipase.
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PROSITE; PS00120; LIPASE_SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:6617; LIPA.
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EMBL;
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                                                                                                                                                                                                                                                                                     208 CPISYLDHVSASFVLRAVAM-----HLDQMLVTMGIHQLNFRSDMGVQIVDSLCD---- 257
                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                                                                                                    HHLFQMIRKGTFAKYDYGLLG-NLRRYGHLRPPAFDLSSIPESLPIWMGYGGLDALADVT 357
                                                                                                                                                                                                                                                                                                                                                                                       294 LHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDMLVPTAVWS--GGHDWLADVY 351
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             42 GSGGL------CDQLLLPLGYPCTEHNVETKDGFLLSLQHIPHG-KNKAADSTGP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pistillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva C., "The Drosophila melanogaster lipase homologs: a gene family with tissue and developmental specific expression."; J. Mol. Biol. 276:877-885 (1998).
                                                                                                                                                                         GPVA----SVAFCTSPMAKLGRLPDHL-------IKDLFGDKEFL
                                                                                                                                                                                                                                                                                                                            258 -----GEHVDCNNLLSAITGENCCF-----NTSRIDYYLEYEPHPSSTKNL
                                                                                                                                                                                                                                                                                                                                          235 PQSAFLKWLGTHVCTHVILKELCG-NLCFLLCGFNERNLNMSRVDVYTTHSPAGTSVQNM
                                                                                                                                                                                                                                              DWSWQELAEYDLLAMIGYVYTVT-QSKILYVGHSQGTIMGLAALT-MPEIVKMISSAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
                                                                                                                                          73;
                                                                                                                      DB 1; Length 399;
                                                                                                                                ; Pred. No. 5.4e-37;
59; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            DVQRTIRELGSTPELLYIGDYGHIDFVMSVKAKDDVYVDLIRFLRE 403
                                                                                                                                                                                                                                                                                                                                                                                                                              352 DVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKIINLMRK 397
                                                                                                   55F27391306B609A CRC64;
                    H -> P (IN CESD).
/FTId=VAR_004248.
H -> R (IN CESD).
/FTId=VAR_004249.
L -> P (IN CESD AND WD).
/FTId=VAR_004250.
                                                                               -> R (IN REF. 3)
                                                                                                               23.5%; Score 515.5; DB 1
          /FTId=VAR_004247
H -> P (IN CESD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Canton-S; MEDLINE=98227315; PubMed=9566193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipase 3 precursor (EC 3.1.1.-).
LIP3 OR CG8823.
                                                                                                   45415 MW;
                                                                                                                                         Matches 131; Conservative
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399 AA;
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                                                                                                                                 Local Similarity
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CONFLICT
SEQUENCE
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046108;
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
By Sutton G.G., Wortnam J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helf G., Champe M., Pfeiffer B.D.,
Ballew R.M., Basu A. An H.-J., Andrews-Ptannkoch C., Baldwin D.,
Ballew R.M., Basu A. Baxendle J., Bayraktaroglu L., Basaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshkov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brother P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
R.A. Berlos B., Delcher A., Deny E.C., Davenport L.B., Davies P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
R.A. Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R.A. Houston K.A., Howland T.J., Wei M.-H., Ibeywan C.,
Alallah M., Ralush F., Karpen G.H., Ke Z., Kenison J.,
R. Minmel B.E., Kodire C.D., Kraff C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lia Y., Mattei B., McIntosh T.C., McIed M.P., Morshrefi A.,
Mount S.M., Wollson P.C., McIed M.P., Morshrefi A.,
R. Houston C., Milshina N.Y., Mobarsy C., Morsis J., Morsh V., Smith T.,
Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,
Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Smith T.,
Shue B.C., Siden Kiamos I., Simpson M., Stupski M.P., Sander S.,
R.A. Wallskas R., Welser J., Weitsenbach J.,
Wang Z.-Y., Wassarman D.A., Weitselbung G.X., Wan G., Sheng X.H., Zhong W., Zhong G.X., Zho O., Zhong Y.,
The genome sequence of Drosophila melanogaster.",
R.The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i - DEVELOPMENTAL STAGE: ONLY AT LARVAL STAGES.
-i - DEVELOPMENTAL STAGE: ONLY AT LARVAL STAGES.
-i - SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC, HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 N-LINKED (GLCNAC. . .) (Po
44901 MW; A718D1D743673802 CRC64;
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EMBL; AE001659; AAF54935.1; -.
FlyBase; FBgn0023495; Lip3.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
InterPro; IPR00379; Ser_estrs_site.
Ffam; PF00561; ashydrolase, 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 513.5; DB
Pred. No. 7.9e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPASE 3
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31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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CARBOHYD
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TISSUE=Liver;
                                                                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                        205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Lysosomal.

TISSUE SPECIFICITY: Expressed at low levels in most tissues. High level expression is found in hepatcoytes and splenic and thymic cells. Very high level expression is observed in cells of the small intestinal villi, the zona fasciculata and reticularis of the adrenal cortex, pancreatic acini, and renal tubular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                       LVMVSERPEYNDKIKSAHLLGPAAYMGNMK-SPLTRAFAPILGQPNAIVEVCGSMEFMPS 229
                                                                                                                                                                                                   LLSLQHIPHGKNKAADSTGPPVFLQHGLFQGGDTWFINSAEQSLGYILADNGFDVWIGNV 129
                                                     RGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGYVYTVT-QSKILYVGHSQGTIMG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                                                        TKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSIPESLPIWMGYGGLDALA
                                                                                                 LAALT-MPEIVKMISSAALLCPISYLDHVSASFVLRAVAMHLDQ----MLVTMGIHQL---
                                                                                                                                           -NFRSDMGVQIVDSLCDGEHVD-CNNLLSAITGENCCFNTSRIDY-YLEY----EPHPSS
                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lysosomal acid lipase/cholesteryl ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterol esterase) (Lipase A) (Cholesteryl esterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (BY
                                                                                                                                                                                                                                  DVTDVQRTIRELG -- STPELLYIGDYGHIDFVMSVKAKDDVYVDLIR 399
                                                                                                                                                                                                                                                       DVSDVRKLRDELPNMALDYLVPFEKWAHLDFIWGTEARKYVYDEVLK 388
                                                                                                                                                                                                                                                                                                              397
                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; C
Rodentia; S
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelium,
                                                                                                                                                                                                                                                                                                              LICH_MOUSE
                                                                                                                                                                                                                                                                                                                          2920M5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CNNLLSAITGEN-CCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVLAPVLSLNF--ASGPLLQLGRLPDPLLKDMFGQKQFLPQSAMLKWLSIHVC--THVIM 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEKNYFHYNOSFPPSYNIKNM--KLPTALWSGGRDWLADINDITILLTQI---PKLVYH 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRRVGSGSGGLCD-----QLLLPLGYPCTEHNVETKDGFLLSLQHIPHG-KNKAADS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER
                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
WH. F886C39E1CCFA91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFWDWSWQELAEYDLLAMLGYVYTVT-QSKILYVGHSQGTIMGLAALT-MPEIVKMISSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLCPISYLDHVSASFVLRAVAMHLDQMLVTM-GIHQLNFRSDMGVQIVDSLCDGEHVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 KELCANVFFLLCGFNEKNLNMSRVDVYTTHCPAELLVQNMLHWGQVFKYRKLQAFDWG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNLRRYGHLR----PPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lysosomal acid lipase/cholesteryl ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase) (Sterolesterase) (Lipase A) (Cholesteryl esterase).
                                                                                                                                                                                                               Glycoprotein; Signal; Lysosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.9%; Score 503; DB 1; 33.8%; Pred. No. 6.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (5-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                    HYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --IGDYGHIDFVMSVKAKDDVYVDLIRFLRE
                                                                                                                InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                      MGD; MGI:96789; Lipl.
InterPro; IPR000073; Abhydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                       S00120; LIPASE_SER; 1.
Lipid degradation; Gl
                                                                                                                                                                 Pfam; PF00561; abhydrolase; 1 PROSITE; PS00120; LIPASE_SER;
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                                              EMBL; Z31689; CAA83494.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                        372
372
34
99
159
271
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397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPA OR LAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Sim
Matches 132;
                                                                                                                                                                                                               Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICH_RAT
Q64194;
                                                                                                                                                                                                                                                                                                                                ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                   J. LIPID RES. 36:2212-2218 (1995).

-1- FUNCTION: CRUCIAL FOR THE INTRACELLULAR HYDROLYSIS OF CHOLESTERYL ESTERS AND TRIGLYCERIDES THAT HAVE BEEN INTERNALIZED VIA RECEPTOR-MEDIATED ENDOCYTOSIS OF LIPOPROTEIN PARTICLES. IMPORTANT IN MEDIATING THE EFFECT OF LID. (LOW DENSITY LIPOPROTEIN) UPTAKE ON SUPPRESSION OF HYDROXYMETHYLGLUTARYL-COA REDUCTASE AND ACTIVATION OF ENDOGENOUS CELLULAR CHOLESTERYL ESTER FORMATION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Lysosomal.
SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHG-KNKAADSTGPPVFLQ--HGLFQGGDTWF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 INSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAML 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 GYVYTVTQSKILY-VGHSQGTIMGLAALT-MPEIVKMISSAALLCPISYLDHVSASFVLR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 AVAMHLDQMLV--TMGIHQLNFRSDMGVQIVDSLCDGEHVD----CNNLLSAITGEN-CC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G----RLPDLLLEDLFGQKQFLPQSAMVKWLSTHIC--THVIMKELCANIFFLICGFNEKN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLG-NLRRYGHLRPPAFDLS 335
                         Nakagawa H., Matsubara S., Kuriyama M., Yoshidome H., Fujiyama J., Yoshida H., Osame M.; "Clonido of rat lysosomal acid lipase cDNA and identification of the mutation in the rat model of Wolman's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Mismatches 154; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                            similarity).
CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
M, 97A38595A0523947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::: ||| ||:||:|| ||:|| || EIIMHWGYP--EHSVQTGDGYILGVHRIPHGRRNQFDKGPKPVYYLQWRHGFLADSSNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 NYILNKTGQEQLYNVGHSQGCTIGFIAFSQMPELAKKVKMFFALAPVLSLNFASGPMVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 LNMSRVDVYTTHCPAGTSVQNMVHWTQVVKYHKLQAFDWGSSDKNYFHYNQSYPPLYSIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipid degradation; Glycoprotein; Signal; Lysosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 486; DB 1;
Pred. No. 1.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S81497; AAB36043.2; -.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
MEDLINE-96129534; PubMed-8576647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45186 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
99
159
271
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319
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
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RA Adams M.D., Celniker S.E., Holt K.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt K.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Mortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Abril J.F., Agbapani A., An H.-J., Andrews-Pfannkoch C., Baladwin D.,
RA Beeson K.Y., Benca M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Beeson K.Y., Benca P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P.,
RA Chorry J.M., Cawley S., Dallike C., Perraz C., Ferriera S., Fleischmann W.,
RA Chodek A., Gong F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Galbart W.M., Calasser R.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glann P., Harris M.,
Alush P., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Minnel B.E., Kodira C.D., Kraft C., Kraft C., Kraft C., Mortis J., Mostrei B.,
Rount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Rabon D.R., Noy M., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,
Rhout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,
Spier E., Sperdeling A.C., Staplecon M., Stupsk M. P., Shu B.,
Rabon D.K., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Rabon D.K., Woodage T., Worley K.C., Wu D., Yang S., Zhu D.,
Rabon D.K., Woodage T., Worley K.G., Wu D., Yang S., Zhu K.,
Rhouck S., Woodage T., Worley K., Siu
                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pistillo D., Manzi A., Tino A., Pilo Boyl P., Graziani F., Malva C.; "The Drosophila melanogaster lipase homologs: a gene family with tissue and developmental specific expression."; J. Mol. Biol. 276:877-885(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPATIC, LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.). ALSO SIMILAR TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- TISSUE SPECIFICITY: OVARIES.
-i- SIMILARITY: PARTIAL WITH OTHER LIPASES (PANCREATIC, GASTRIC,
                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:2185-2195(2000).
-!- FUNCTION: COULD BE A DIGESTIVE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98227315; PubMed-9566193;
                                                                                                                                                                                                                                                                                Lipase 1 precursor (EC 3.1.1.-).
LIP1 OR CG7279.
                                                                                                                                                             LIP1_DROME STANDARD; F (046107; 09VKR6; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequing-15-JUN-2002 (Rel. 41, Last annotations)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 7-433 FROM N.A.
                           385 LYNEVVSLMKK 395
393 VYVDLIRFLRE 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Query Match
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Matches
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRKMFPVILGHYPAGVAAKQVKHFIQIIKSGRFAPYSYSSNKNMQLYRDHLPPRYNLSLV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 PESLPIWMGYGGLDALADVTDVQRTIRELGST--PELLYIGDYGHIDFVMSVKAKDDVYV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTGPPVFLQHGLFQGGDTWFIN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPNVSLAYLLADHNYDVWLGNARGNRYSRNHTTLDPDESKFWDFSWHEIGMYDLPAMIDH 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEM (BY SIMILARITY).

(POTENTIAL).

(POTENTIAL).

(POTENTIAL).

(POTENTIAL).

(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AMHLDQMLVTMGIHQL----NFRSDMGVQIVDSLC----DGEHVDCNNLLSAITGENCC-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLYFNS-LVGSSIREMFNGEFR-----FLCRMTEETERL-CIEAVFGIVGRNWNEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9E32E20BEAE93E3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SURRED GLANGE RELAY SYSTEM (BY SULINKED (GLCNAC...) (EN LINKED (GLCNAC...) (FOR ALLINKED (GLCNAC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipid degradation; Signal; Glycoprotein.
1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1;
2.7e-29;
  LEPIDOPTERAN EGG-SPECIFIC AND YOLK PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 28, Created)
(Rel. 28, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%; Score 427;
                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000073; Abhydrolase.
InterPro: IPR000734; Lipase.
InterPro: IPR0007379; Ser_estrs_site.
Pfam; PP00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPASE 1.
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                                                                                                                                                                                                                                                                                                    AAF52994.1; -.
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                                                                                                                                                                                                                                                                           EMBL; Y14366; CAA74736.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                          EMBL; AE003629;
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P34163;
01-FEB-1994
01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=92245761; PubMed=1574929; Abraham P.R., Mulder A., Van'T Riet J., Planta R.J., Raue H.A.; Abraham P.R., Mulder A., Van'z Riet J., Planta R.J. k segment of "Molecular cloning and physical analysis of an 8.2 kb segment of chromosome XI of Saccharomyces cerevisiae reveals five tightly linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | : : | | :: | | : : | 343
K-ILENWKSFNILPRQKIASYAKLY-STTSVKSIVHWFQILRSQKFQMFEESDNMLNSLT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rad M.R., Xu G., Kirchrath L., Fritz C., Keuchel H., Hollenberg C.P.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 HDLGYDVWMGNNRGNKYSTAHLNKPPKSNKFWDFSIDEFAFFDIPNSIEFILDITKVDKV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYVGHSQGTIMGLAALTMPEIVKMISSAALLCPISYLDHVSASFVLRAVAMHLDQMLVTM 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHNVETKDGFLLSLQHIPH-GKNKAADSTGPPVFLQHGLFQGGDTWFIN-SAEQSLGYIL 117
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                                                                                                                                              Saccharomycetes;
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InterPro: IPR00379; Ser_estrs_site.
Pfam: PF00561; abhydrolase; I.
Hydrolase: Libid degradation.
SEQUENCE 548 AA; 62979 MW; 32D1F230701CB083 CRC64;
                                       3.1.1.-)
                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccl
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 293.5; DB 1; 24.8%; Pred. No. 1.2e-17; ive 67; Mismatches 136;
15-JUN-2002 (Rel. 41, Last annotation update)
Triglyceride lipase-cholesterol esterase (EC. TGL1 OR YKL140W OR YKL5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIHQLNFRSDMGVQIVDSLCDGE-------
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395 EHLDLIWGKDADTLVIAKVLRFI 417
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PIR; S39000; S39000.
SGD; S0001623; TGL1.
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hes 95; Conserv
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                                                                                                                                                                                                                                                                                                                    Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oeffner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 TKDGFLLSLQHIPHGKNKAADSTGPPVFLQHGLFQGGDTWFIN------SA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
STRAIN=KIZ / MG1655;
PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAEYDLLAMLGYVYTVTQSKILYVGHSQGTIMGLAALTMP------EIVKMISSAALLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 KLGTFSISYNDDR-----RYNSHYYTA----DYYQNVYSGTFG--SLGLRAGIQRYNNGD
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Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 841;
                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
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D2016BB0ACD726AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 107.5; 22.3%; Pred. No. 0.2
                                                                            protein yagx precursor
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ne; EG13563; yagx.
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                      Escherichia coli.
                                                                                                                                             NCBI_TaxID=562;
                                                                                           YAGX OR B0291
                                                                              Hypothetical
YAGX_ECOLI
ID YAGX_ECOLI
AC P77802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 LLAMLGYVYTVTQSKILYVGHSQGTIMGLAALTMPEIVKMISSAALLCPISYLDHVSASF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 TSRIDYYLEYEPHPSSTKNL------HHLFOMIRKGTFAK-----YDYGLLGN-- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNANTGKYIALDLSLPLGNWFSAGMTHQNGYTMANLSARKQFDEGTIRTVGANLSRAISG 604
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LLFLLVLSFTLVESVYQY-----QILILEPIYRFTDSAAVPAKSIYFTNLPQHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: STRONG, TO C.ELEGANS F40H6.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LRRYGHLR------PPAFDLSSIPESLPIWMGYGGLDALADVT 357
                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 133.3 kbg protein F40H6.5 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B5C30EBDA014D793 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                            PRT; 1216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1216 AA; 133313 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; F40H6.5; CE01937.
InterPro; IPR004024; DUF225.
InterPro; IPR001079; Galectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U21310; AAA62522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02795; DUF225; J
SMART; SM00276; GLECT; 1
Hypothetical protein; Tr:
TRANSMEM 3
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
397
460
801
1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                          DYG 379
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Cambillau C.;
                                                                                                                                                                                                                               LIPP_HORSE
P29183;
                                                                                                                                                 360 QR 361
                                                                                                                                                                       495 SQ 496
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                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHSTFSVHDKLFWDWSWQELA------EYDL-----LAMLGYVYT---VTQSKI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYVGHSQGTIMGLAALTMPEIVKMISSAALLCPISYLDHVSASFVLRAVAMHLDQMLVTM 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 IHTYHTEGAGGGHA----PDIIKICGELNVL-PSS--TNPTRPYTINTLEHLDMLMVCH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHGKNKAADSTGPPVFLQHGLFQGGDTWFINSAEQSLGYILADNGFDVWIGNVRGTRWSK 136
                                                                                                                                                 MEDIURE-97061201; PubMed-8905231; MEDIURE-97061201; PubMed-8905231; MEDIURE-97061201; PubMed-8905231; MEDIURE-97061201; MEDIURE-97061201; MEDIURE-97061201; MEDIURE T., MITCOSAWA M., SUGIUTA M., SASAMOCO S., Kimura T., HOSOUCHI T., MATERIA A., NARAZARI N., NARUO K., Choumura S., Shimpo S., Tabeta S.; Wada T., Watanabe A., Yasuda M., Tabata S.; Che genome of the unicellular cyanobacterium "Sequence analysis of the genome of the central sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.",
                                                                                                                                                                                                                                                                  PAAGTKATTCT-PGAWNIHRMLQAADGFPIN----LGFLGKGNG-----SQPAALAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 QIKAGAIGLKLHEDWGTTPAAIDNCLGVAEDYDVQVAIHTDTLNEAGFVETTIAALKNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 135; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (BY SIMILARITY).
2 (BY SIMILARITY).
1 AND 2 (BY SIMILARITY).
1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 97.5; DB 1; Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NICKEL 2 (BY SIMILARITY).
NICKEL 2 (BY SIMILARITY).
NICKEL 1 AND 2 (BY SIMILAR.
NICKEL 1 (BY SIMILARITY).
NICKEL 2 (BY SIMILARITY).
NICKEL 2 (BY SIMILARITY).
BY SIMILARITY
                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
UREC OR SLL1750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
1C720A254335D7FD CRC64;
                                                                                                      Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD002467; UreaseA; 1.
PROSITE; PS00145; URBABE_2; 1.
PROSITE; PS01120; URBASE_1; 1.
Hydrolase; Metal-binding; Nickel; Complete
                     569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.4%; Scc
19.6%; Pre-
tive 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001924; UreaseA. Pfam; PF00449; urease; 1. Pf02802; urease_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61037 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90903; BAA17083.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
274
362
322
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274
362
322
569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; M38.UNW;
                                                                                                                             NCBI_TaxID=1148;
                    URE1_SYNY3
P73061;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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RESULT 13
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triacylglycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic lipase) (PL) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρλ
                                                                                                                                                                                                                                                                               -----KYDYGLLGNLRRYGHLRPPAFDLSSIPESLPIWM-----GYGGLDALADVTDV 359
                                                                                                                                                                                                                                                                                                                                      438 SPAFFGVKPELVIKGGIVAYAQMGDAN---ASIPTPQPVHMQPMFANYGGAIAATSVTFV 494
                                                              379
                                                                                                                                                                                                         380 AHKMKVQRGQLPGETGNNDNLRAKR--YVAKYTINPAITHGISEEIGSVEVGKLADLCLW 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-92267022; PubMed=1587279;
MEDLINE-92267022; PubMed=1587279;
MECHELEC B., Foglizzo E., Bonicel J., Bougis P.E., Chapus C.;
"Sequence of horse pancreatic lipase as determined by protein and CDNA sequencing. Implications for p-nitrophenyl acetate hydrolysis!
                                                                  323 HLHR-NIPED--VAFAESRIRRETIAAEDILHDLGAFSIISSDSQAMGRVGEVICRTWQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 238:709-732(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horse pancreatic lipase. The crystal structure refined at 2.3-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00151; lipase; 1.
Pfam; PF01477; PLAT; 1.
SMART; SMOA308; LH2; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Pancreas; Signal; 3D-structure.
                                                                                                                                       -----TGENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bourne Y., Martinez C., Kerfelec B., Lombardo D., Chapus C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
GIHQLNFRSDMGVQIVDSLCDGEHVDCNNLLSAI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000734; Lipase.
InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-94238688; PubMed-8182745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic lipases.";
Eur. J. Biochem. 206:279-287(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X66218; CAA46961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S21223; S21223.
1HPL; 31-MAY-94.
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 chem. Biophys. Res. Commun. 188:964-971(1992).
CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol + a
fatty acid anion.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N------LCENLFOVETVNCICVDWKGGSRT-----TYPQATQNIRIVGAEVAYL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HNVETKDGFLLSLQHIPH-----GKNKAADSTGPPVFLQHGLF-QGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 KIVNTR--FLLYTNENPNNFQEISADASTIRGSNFRTDR--KTRFIIHGFTDKGEENWLS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D--SLCDG--EHVDCNNLLS-----RITGENC-----CFNTS----RI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 SKOYEIFTGLLKPGDTHLNE-------FDSDVDVGDVQKVKFVWYNNVINPTLP 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 IVRLDPSDAQFVDVIHTDAAPMVPNLGFGMSQTVGHLD-FFPNGGKEMPGCQKNVLSQIV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::| :| ||-|| ::
| DINGVWEGTRDFVACNHLRSYKYYADSIVNPNGFAGFSCASYTAFSANKCFPCSNGCPQM 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHYA--DRFSRKTDGVGQTFYLNTGDSSNFARWRYQVAVTLSGRRVTGHVLVSLYGSKGN 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 LRRY----GHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQR------TIR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ALPLILLVVS------CCGRIVSGASPAAALRRVGSGSGGLCDQLLLPLGYPCTE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ALPLLLGAVAGLEVCYERLGCFGNRI-------PWSGGTLERPFSTL--PSTP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQEL----AEY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 -- DLLAMLGYVYTVTQSKILYVGHS-------QGTIMGLAALT------MPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVKMISSAALLCPISYLDHV----SASFVLRAVAMHLDQMLVTMGIHQLNFRSDMGVQIV
                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches 168; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 465;
                                                                                                                                                                                                                                                                                                                                                                            THACYLGIVCEROL LIPASE, PRITACYLGIVCEROL LIPASE, PRITACYLGIVCEROL LIPASE, PRICHAGE RELAY SYSTEM (BY SICHARGE RELAY SYSTEM (BY SICHARGE RELAY SYSTEM (BY SICHARITY.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.
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47F53275997BBA19 CRC64;
                                                                                                                                                                                                                                                                                                        PRINTS; PRO0821; TAGLIPASE.
SMART; SM00308; LH2; 1.
PROSITE; PS00120; LIPASE_SER; 1.
Hydrolase; Lipid degradation; Pancreas; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 DYYLEYEPHPSSTKNLHHLFQMIR--KGTFAKYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94; DB 1;
Pred. No. 1.7;
                                                                                                                                                                                                                                        Interpro; IPR000734; Lipase.
Interpro; IPR001024; Lipoxygenase_LH2.
Interpro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 B)
51161 MW;
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                                                                                                                                                                                                                                                                                  Pfam; PF00151; lipase; 1. Pfam; PF01477; PLAT; 1.
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281
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194
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303
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01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Triacylgycerol lipase, pancreatic precursor (EC 3.1.1.3) (Pancreatic
                                                                                                                                                                                                                                                                                                                                                              INSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLL--A 163
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                                                                                                                                                                                80% LOSS OF P-NITROPHENYL ACETATE
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                                                                                                                                                                                                                                                                                                                               PWSPEKVNTR--FLLYTNENPDNFQEIVADPSTIQSSNFNTGRKTRFIIHG-----F
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                               PANCREATIC
                                                                                                                                                                                                                                                                     Mismatches 155; Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93075235; PubMed=1445366;
Aleman-Gomez J.A., Colwell N.S., Sasser T., Kumar V.B.;
"Molecular cloning and characterization of rabbit pancreatic
Lighyceride lipase.";
                                                                                                                                                                                                                                           Length
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                                                                                                                                                                             S->X: 80% LOSS OF P-NITRO
HYDROLYSIS ACTIVITY.
382F33F3CE446738 CRC64;
                             TRIACYLGLYCEROL LIPASE,
                                          CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                     4.4%; Score 95.5; DB 1; 20.7%; Pred. No. 1.2; tive 56; Mismatches 155;
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                                                                                                                                                                                                          461 AA;
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Q02157;
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Search completed: December 30, 2002, 20:44:30 Job time : 41 secs

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096192 homo sapien 090kt5 drosophila 090kt5 drosophila 090kt9 drosophila 09533 caenorhabdi 09573 caenorhabdi 09776 drosophila 09776 drosophila 09746 drosophila 09745 drosophila 09745 drosophila 09745 drosophila 0917219 bombyx mori 0917219 bombyx mori 0917219 drosophila 0917219 drosophila 0917219 drosophila 0917219 drosophila 0917219 drosophila 0917210 drosophila

Run on:

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STRAIN-CV. COLUMBITA;
MEDLINE-20083487; PubMed=10617197;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adms M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzbarg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC006298; AAD25569.1; -.
InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser.—sstrs_site.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 344 Aa, 38868 MW; 7BC4ED067E3602C4 CRC64;
                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative lysosomal acid lipase.
AT2G15230.
                                                                                                                                                                                                                                                   ALIGNMENTS
                     Q9D6L9
Q9D6Q3
Q9D766
Q9CPP8
Q9D6M9
                                                                                                                                                                                                                                                                                           PRT;
                                                                     Q96LG2
017766
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09VKT9
020449
095X33
094252
094252
09V796
09VBKG
09VBKT2
09VKT2
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094568
090276
090KT0
                                                                                                                                                                                                                          09VG46
                                                                                                                                                                                    Q9VKT7
 Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                          PRELIMINARY;
[2]
SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
NCBI_TaxID=3702;
417
416.5
412.5
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392.5
384.5
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Q9SKL5;
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Q9SKL5
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051kv1 caenorhabdi
061866 caenorhabdi
0916956 caenorhabdi
093789 caenorhabdi
096fmt3 arabidopsis
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918.253 Million cell updates/sec
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                                                                                                    1 MAMAGHAPGGALPLILLVVS......DDVYVDLIRFLRENGWHNSY 410
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                                                    December 30, 2002, 20:09:51; Search time 92 Seconds
                                                                                                                                                            671580
      5.1.3
Compugen Ltd.
                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                           671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
      GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     protein search, using sw model
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0616956
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_rodent:*
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sp_vertebrate:*
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sp_phage:*
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seq length: 2000000000
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sp_bacteria:*
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Database

Result Š.

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77339 MW; 85D3F46C9DE81F61 CRC64;
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630 ARKEIYDKIINTIK 643
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
  684 AA;
                                                          Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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SEQUENCE
                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                          280 SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSIPE 339
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                                         Gaps
                                                                                                    40 GSGSGCLCDQLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTGPPVFLQHGLFQ 99
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
Length 344;
                                       71; Indels
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InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
InterPro; IPR000734; Lipase.
InterPro; IPR0007379; Ser_estrs_site.
Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid Y57E12B."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095XV1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
101-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 77.3 kDa protein.
48.1%; Score 1055; DB 10; 54.5%; Pred. No. 1.2e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              684 AA
                                         42; Mismatches
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STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                    al Similarity 54.5
198; Conservative
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"Direct Submission.";
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  Query Match
                    Best Local
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG----PPVFLQHGLFQGGDTW 104
                                                                                                                                                                                                                           105 FINSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAM 164
                                                                                                                                                                                                                                                                                                                                     LGY-VYTVTQSKILYVGHSQGTIMGLAALTM-PEIVKMISSAALLCPISYLDHVSASFV- 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSI 337
                                                           Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              222 LRAVAMHLDOMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD---CNNLLSAITGENC-CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
     DB 5; Length 684;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067942; AAG45574.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
2K6.7.
26.0%; Score 571.5; DB 5; 33.7%; Pred. No. 1.1e-43; tive 75; Mismatches 144;
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InterPro; IPR000379; Ser_estrs_site.
PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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STRAIN=BRISTOL N2;
MEDLINE=99069613; Pubmed=9851916;
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Length 404;

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45779 MW; A87561AE0B2FED46 CRC64;
  404 AA;
                                  Similarity
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                                   Best Local Sim
Matches 121;
  SEQUENCE
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                       Query Match
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                                                               49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                          NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                             381
                                                                                                                                                     167 YVYTVT-QSKILYVGHSQGTIMGLAALTMPE--IVKMISSAALLCPISYLDHVSA--SFV 221
                                                                                                                                                                                                                                         CCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDL 334
                                            Gaps
                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                222 LRAVAMHLDQMLVTMGIHQL---NFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-EN
                                                                                                                                                                                                                                                                                     SSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELL------YIGDYGHI
                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                     Length 403;
                     Query Match 25.4%; Score 557.5; DB 5; Length Best Local Similarity 32.4%; Pred. No. 9.4e-43; Matches 124; Conservative 65; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF022976; AAC69088.2; -InterPro; IPR000734; Lipase. InterPro; IPR000734; Lipase. InterPro; IPR000379; Ser_estrs_site. PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Bavidson S., Wohldmann P., Bauer C.;
"The sequence of C. elegans cosmid R11G11.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 45704 MW; 7F5622F820C5FE52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
10-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypotherical 45.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                          404 AA
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STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                         328 TAI-KGTKIYLYWSDADWLADTPDV---
                                                                                                                                                                                                                                                                                                                                           | | :: | | |: | :: | DETWGLRAPDDIYRPAIKLCTDD 399
                                                                                                                                                                                                                                                                                                                               DFVMSVKAKDDVYVDLIRFLREN 404
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 403 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BRISTOL N2; Waterston R.;
 SEQUENCE
                                                                                                          107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 DQWNSTRVPVYASHDPAGTATQNIVHWIQMVRHGGVPAYDWGSKENKKKYGQANPPEYDF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELL----YIGDYGHIDFVMSVKAK 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| : | :| || || || :: | 329 TAI-KGTQIYLYWSDADWLADKTDITNYLL-TRLNPAIIAQNNYFTDXNHFDFVFGLRAP 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                         49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                         Gaps
                                                                                                                                                                                                                      107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                     167 YVYTVT-QSKILYVGHSQGTIMGLAALTMPE--IVKMISSAALLCPISYLDHVSA--SFV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                            222 LRAVAMHLDQMLVTMGIHQL---NFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-EN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 CCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDL 334
                                                                                                                                            Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                  152 KVLEVTGQESLYYMGHSQGTLTMFSHLSKDGIFAKKIKKFFALAPVGSVKDIKGFLSFF
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31.9%; Pred. No. 5.7e-42;
ive 72; Mismatches 152; Indels
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percy C.M., Lloyd C.R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; 279696; CABOL973.1: -
InterPro: IPRO00073; Abhydrolase.
InterPro: IPRO00734; Lipase.
InterPro: IPRO007379; Ser_estrs_site.
Pfam: PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SEQUENCE 405 AA; 45790 MW; FFCAA9E49A782A60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
25.0%; Score 549.5; DB 5; 32.9%; Pred. No. 5.1e-42; iive 68; Mismatches 156;
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Matches 121; Conservative
                                                         Conservative
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SEQUENCE 1
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2010 (TrEMBLrel. 16, Last sequence update)
01-MAR-2010 (TrEMBLrel. 16, Last annotation update)
Similarity to lipase.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                      338 PESLPIWMGYGGLDALADVTDVQRTIRELGSTPELL------YIGDYGHIDFVM 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                •103 TWFINSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
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                                                                                                                                                                                                                                             --NRPVYLYWGDSDWLADPTDV-----TDFLLTHLNPSTVVQNNKLIDYNHLDFIW 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
                                     273 NATRVPIYVAHTPAGTSTQNIVHWIQMVRHGGTPKYDYGEKGNKKHYGQANVPAYDFTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VSASFVLRAVAMHLDQMLVTMGIHQLNFRSDMGVQIVD
QIIMRWGYPAMIYDVTTEDGYILELHRIPYGKTNVTWPNGKKPVVFMQHGLECSSSNWVV
                                                                        167 YVYTVT-QSKILYVGHSQGTIMGLAALTMPEI--VKMISSAALLCPISYLDHVSAS--FV
                                                                                                153 KALEVTGQDSLYYIGHSQGTLTMFSRLSEDKVGWGNKIKKFFALAPVGSVKHIKGALKFF
                                                                                                                                                                     NTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLGNLRRYGHLRPPAFDLSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AMLGYVYTVTQSKILYVGHSQGTIMGLAALTMPEIV----KMISSAALL-----CPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 PHDHRHRRYRRKNLPRRVMKITCLSSFKNRP-PLFLDGQSLTRKVG------DFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLCDGEHVDCNNLLSAITGENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKY
                                                                                                                        LRAVAMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD---CNNLLSAITG-ENCCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.6%; Score 540; DB 10; 35.3%; Pred. No. 2.7e-41; ive 54; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                         318 AA
                                                                                                                                                                                                                                                                                                                                                         PRT;
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MEDLINE-98162728; PubMed-9501997;
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36448 MW;
                                                                                                                                                                                                                                                                                   382 GLRAPKDIYEPIIDIVRND 400
                                                                                                                                                                                                                                                                   386 SVKAKDDVYVDLIRFLREN 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 4:401-414(1997).
EMBL; AB007650; BAB08297.
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Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 AA;
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Tabata S.;
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NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN 265
314 DYGLLG-NLRRYGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELG----S 368
                                        :|| |:: || |||:::|:|| |||:::|22 NYGSSDRNIKHYGQAIPPAYNISAIPHELPLFFSYGGLDSLADVKDVEFLLDOFKYHDID 281
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 539; DB 11;
33.6%; Pred. No. 4.6e-41;
iive 68; Mismatches 135;
                                                                                                                                                                                    282 KMNVQFVKDYAHADFIMGVTAKDVVYNQVATFFK 315
                                                                                                                                            369 TPELLYIGDYGHIDFVMSVKAKDDVYVDLIRFLR 402
                                                                                                                                                                                                                                                                                                                                                                                            395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; PubMed=11217851;
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InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
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PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44603 MW; D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2002 (TrEMBLrel. 20, 2310051B21Rik protein.
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Matches 129; Conserv
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NCBI_TaxID=10090;
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01-JUN-2001
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A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ashurner M., Batalov S., Casavant T., Ashurner M., Batalov S., Casavant T., Racita M., Stauda H.A., Staubi F., Sisi C., King B., Kochiwa H., Ashim P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ashair M., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Bronstein M.J., Bult C., Fletcher C., Fultta M., Gariboldi M., A Bronstein M.J., Bult C., Fletcher C., Fultta M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiga M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Schochach R., Schoenbach C., Schoenbach C., Sulting L., Mahttaker C., Wiltraker C., Wilming L., Myshiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Angarabali S., Manachi S., Hanselia V., Kawaji H., Kohtsuki S.,
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  -- EVCSRELLDLLCSN 256
                                                                                                              371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR
                                           YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---1GDYGH
                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 395;
                                                                                                                                                                                                                                                             01-50N-2001 (TrEMBLrel. 17, Created)
01-50N-2001 (TrEMBLrel. 17, Last sequence update)
01-50N-2002 (TrEMBLrel. 20, Last annotation update)
Adult male tongue CDNA, RIKEN full-length enriched library,
clone:2310079020, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.6%; Score 539; DB 11; Length 3 33.9%; Pred. No. 4.6e-41; ive 66; Mismatches 136; Indels
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                                                                                                                                                                                                                                       395 AA.
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LIPKFLLKVIFGNKMFMPHNYLDQFLGT---
                                                                                                                                                         IDFVMSVKAKDDVYVDLIRFLREN 404
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InterPro; IPR000379; Ser_est
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                                                                                                                                                                                                                                      PRELIMINARY;
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215
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Rawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ashiburner M., Batalov S., Yamanaka I., Radota K., Matsuda H.A., Ashiburner M., Batalov S., Casavant T., Ra Kuehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schim L., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schim L., M., Staubli F., Szuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Okido T., Futuno M., Anon H., Baldarelli R., Barsh G., Browstein M.J., Bult C., Fletcher C., Fujita M., Ganaldo M.F., Rowstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Loons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Rayashizaki Y.
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                                                                                                                                                                                                                                                                                                                     257 ALFIFCGFDKKNLNVSRFDVYLGHNPAGTSTQDLFHWAQLAKSGKLQAYNWGSPLQNLLH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                        | || :|:|:| : :| || || || || || 317 YNQKTPPYYDVSAMTVPIAVW--NGGHDILADPQDVAMLLPKL---PNLLYHKEILPYNH 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
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                                LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR
YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA----
                                                                                                                                      ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
                                                                                                                                                                                                        215 LIHKFLLKVIFGNKMFMPHNYLDQFLGT-------EVCSRELLDLLCSN
                                                                                                                                                                                                                                                                                                                                                                                                                YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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395 AA; 44748 MW; 3ED43992458DE058 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 11;
5.7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%; Score 538; 34.1%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR000734; Lipase.
InterPro, IPR000379; Ser_estrs_site.
Pfam; PF00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 LDFIWAMDAPQEVYNEIVTMMAED 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 IDFVMSVKAKDDVYVDLIRFLREN 404
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EMBL; AK009359; BAB26240.1;
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17,
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Matches 131; Conservative
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                                                                                                                                                                                                 215 FIPKFLLKVIFGNKMFMPHNYLDQFLGT------EVCSRELLDLLCSN 256
                                                                                                                                                                                                                                                                                                              YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGH 380
                                                                                                                                                                                                                                                                                                                                   167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPIS---YLD-----H 215
                                                                                                                                                                                                                                              266 LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR 323
                                                NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                   ALFIFCGFDKKNLNVSRFDVYLGHNPAGTSTQDLFHWAQLAKSGKLQAYNWGSPLQNMLH
                                                                                                                                                                                  216 VSASFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK010139; BAB26725.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-000-2001 (TrEMBLrel. 17, Created)
01-000-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 20, Last annotation update)
Adult male tongue CDNA, RIKEN full.length enriched library,
clone:2310069P19, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA.
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Interpro; IPR000379; Ser_estrs_site.
Pfam; Pf00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                  372 LDFIWAMDAPQEVYNEIVTMMAED 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK010139; BAB26725.1; -.
MGD; MGI:1914967; 2310051B21Rik.
InterPro; IPR000073; Abhydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Q9D6P3
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                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 ALFIFCGFDKKNLNVSRFDVYLGHNPAGTSTQDLFHWAQLAKSGKLQAYNWGSPLQNMLH 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                        107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                                                                                                                                                                                                                                                                                                                                        ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                              167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA-----
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                                                                                                                  52;
                                                         Length 395;
                                                                                                                      Indels
E48A73CCCBFD359D CRC64;
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Last annotation update)
                                                                                                                         66; Mismatches 136;
                                                            24.5%; Score 538; DB 11; 33.9%; Pred. No. 5.7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=TONGUE;
MEDLINE=21085660; PubMed=11217851;
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EMBL; AK009537; BAB26346.1; -.
44651 MW;
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2310051B21RIK.
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395 AA;
                                                                                            Best Local Similarity
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                                                                                                                      Matches 130;
                                                                   Query Match
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Matches 129;
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ANDLINE=2108560; PubMed=11217851;

ARANA J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawa J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Balalov T., Casaront T.,

Radota K., Matsud H.A., Gissi C., King B., Kochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Saki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                              QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
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                                                                                                                                   Gaps
                                                                                                                                                                           NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG
                                                                                                                                                                                                                                                                      167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA-----
                                                                                                                                                                                                                                                                                                 FIVORTGOEKIHYVGHSQGTAIGFIAFSTNPALAKKIKRFYALAPVATVKYTESPFKKIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                   52;
                                                                                                          Length 395;
                                                                                                                                   Indels
                                  InterPro; IPR000379; Ser estrs_site.
Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 Aa; 44607 MW; E43317C2254FA8FB CRC64;
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                                                                                                                                  67; Mismatches 136;
                                                                                                        DB 11;
                                                                                                        24.5%; Score 537; DB 1 33.6%; Pred. No. 7e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 LDFIWAMDAPQEVYNEIVTMMAED 395
         InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
MGI:1914967; 2310051B21Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                       Query Match 24.5
Best Local Similarity 33.6
Matches 129; Conservative
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Q9D6X0
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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishli Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Salio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salio R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
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   Wilming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 LIPKFLLKVIFGNKMFMPHNYLDQFLGT------EVCSRELLDLLCSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmin
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.
                                                            Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 395;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Adult male tongue CDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                  Nature 409:885-690(2001).

EMBL: AR009975; BAB26556.1; -

MGD: MGI:1914967; 2310051B21Rik.

InterPro; IPR0000734; Lipase.

InterPro; IPR000734; Lipase.

InterPro; IPR000379; Ser_estrs_site.

Pfam; PF00561; abhydrolase; 1.

PROSITE; PS00120; LIPASE_SER; 1.

SEQUENCE 395 AA; 44665 MW; 40CA6B67859A8C5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%; Score 537; DB 11; 33.6%; Pred. No. 7e-41;
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STRAIN-C57BL/6J; TISSUE-TONGUE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 LDFIWAMDAPQEVYNEIVTMMAED 395
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2310051B21RIK.
Mus musculus (1
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Rhipg B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 ALFIFCGFDKKNLNVSRFDVYLGHNPAGTSTQDLFHWAQLAKSGKLQAYNWGSPLQNMLH 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 YNQKSPPYYDVSAMTVPIAVW--NGGHDILADPQDVAMLLPKL---PNLLYHKEILPYNH 371
                                                                                                                                                                                                                                                                                                                                                              49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 FIVOKTGQEKIHYVGHSQGTTIGFIAFSTNPALAKKIKRFYALAPVATVKYTESPFKKIS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE-TONGUE;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                                                                                                                                                                              107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                  Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                        DB 11; Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNAR-2002 (TrEMBLrel. 10, Last annotation update)
Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310065807, full insert sequence.
                                                                                                                                                                                                                                                                            D3F96DB83161C3EF CRC64;
                                                                                                                                                                                                                                                                                                                                   67; Mismatches 136;
                                                                                                                                                                                                                                                                                                        24.5%; Score 537; DB 1
33.6%; Pred. No. 7e-41;
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NATURE 409:685-690(2001)
EMBL; AK009990; BAB26629.1; ...
MGD; MGI:1914967; 2310651821Rik.
InterPro: IPR000073; Abhydrolase.
InterPro: IPR00073; Ser_estrs_site.
Pfam; PF00561; abhydrolase: 1.
PROSITE; PS00120; LIPASE_SER: 1.
SEQUENCE 395 AA; 44623 MW; D3F96DB
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                                                                                                                                                                                                                                                                                                                       Similarity
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SEQUENCE FROM N.A.
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Q9D6S5
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Ksukwa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Futcher C., Tomita M., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fetcher C., Fujita M., Gariboldi M., Loons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wishbaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Maraki S., Manaka, V., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGH 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
BABLS AK010026; BAB26651.1; -.
MGD; MGI:1914967, 23100151B21Rik.
InterPro; IPR000734; Lipase.
InterPro; IPR000734; Lipase.
InterPro; IPR000739; Ser_estrs_site.
Pfam; PF00561; abhydrolase, 1.
PROSITE; PS00120; LipASE_SER; 1.
SEQUENCE 395 AA; 44650 MW; 03F16D53373A4D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 395;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Adult male tongue cDNA, RIKEN full-length enriched library,
clone:2310074E21, full insert sequence.
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33.6%; Pred. No. 7e-41;
Live 67; Mismatches 136;
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Matches 129; Conservative
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C STRAIN-C57BL/63: TISSUE-TONGUE;

X RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalow S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalow S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalow B., Kochiwa H.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Mombaerts P.,

Ruschinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyashaw-Boris A., Yoshida K., Wasejawa Y., Kawaji H., Kohtsuki S.,

Nyashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 YVYTVT-QSKILYVGHSQGTIMG-LAALTMPEIVKMISSAALLCPISYLDHVSA---- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SFVLRAV-----AMHLDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.5%; Score 537; DB 11; Length 395; 33.6%; Pred. No. 7e-41; ive 68; Mismatches 135; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 395 AA; 44761 MW; 13889361DC8F17B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL, AK010148; BAB26733.1; -..
MGD: MGI:1914967; 2310051B21Rik.
InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
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Matches 129; Conservative
                    NCBI_TaxID=10090;
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Search completed: December 30, 2002, 20:46:14

Job time : 93 secs

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399 RFLREN 404
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US-09-186-489-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 17, A sequence 3, Ap Sequence 5, Ap Sequence 5, Ap Sequence 6, Ap Sequence 18, A Sequence 18, A Sequence 6, Ap Sequence 2, Ap Sequen
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Seguence 16,
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2194
1 MAMAGHAPGGALPLILLVVS......DDVYVDLIRFLRENGWHNSY
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-232-519-2
US-08-456-956-2
US-08-985-492-15
US-08-750-141A-2
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US-08-227-108-16
US-08-227-108-17
US-09-073-674-17
US-09-073-674-17
US-09-027-108-3
US-09-820-001-2
US-09-820-001-2
US-09-820-001-2
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US-09-036-987A-6
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-08-779-046-2
-08-881-340-2
-08-232-519-2
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 6, Appli	Sequence 70, Appl	•	•	Sequence 86, Appl	Sequence 86, Appl	86,	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli		Sequence 3218, Ap	Sequence 3, Appli	ñ	Sequence 26, Appl	26,	Sequence 26, Appl	Sequence 8, Appli
US-09-355-166-6	US-08-350-884-70	US-08-709-173-70	US-08-709-177-70	US-08-350-884-86	US-08-709-173-86	US-08-709-177-86	US-09-053-866-2	US-09-479-130-2	US-09-087-277-2	US-09-658-499-2	US-09-134-001C-3218	US-08-920-095-3	PCT-US96-05800-3	US-08-467-822-26	US-08-432-697-26	US-08-466-248-26	US-08-448-170-8
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298	989	989	989	841	841	841	382	385	878	878	906	995	266	569	569	569	1227
4.0	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9
87.5	98	98	98	98	98	98	82	85	82	82	85	84.5	84.5	84.5	84.5	84.5	84.5
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## ALIGNMENTS

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APPLICANT: Cibak, Paul L.
APPLICANT: Cibak, Paul L.
APPLICANT: Cibak, Paul L.
APPLICANT: Scharpf Jr., Lewis G.
TITLE OF INVENTION: Purified Recombinant Kid Pregastric Esterase, and
TITLE OF INVENTION: Processes for its Production and Use
FILE REFERENCE: 5499/3
CURRENT FILIAG DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0 26.0%; Score 571; DB 4; Length 378; 35.5%; Pred. No. 1.1e-53; ive 66; Mismatches 154; Indels Sequence 2, Application US/09186489 Patent No. 6375947 Conservative ; ORGANISM: Kid (Goat) US-09-186-489-2 Similarity SEQ ID NO 2 LENGTH: 378 130;

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107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFW-DWSWQELAEYDLLAML 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVPQSLFKFIFGDKIFYPHNFFDQFLAT---------EVCSREMLNLLCS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 GYVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 NALFIICGFDSKNFNTSRLDVYLSHNPAGTSVQNMFHWTQAVKSGKFQAYDWGSPVQNRM 298
299 HYDQSQPPYYNVTAMNVPIAVW--NGGKDLLADPQDVGLLLPKL---PNLIYHKEIPFYN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 380;
                                                                                                                                                                                                                             APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.4%; Score 535.5; DB 2; 33.8%; Pred. No. 8.6e-50; tive 70; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5072-D1-66-TMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                              Warner-Lambert Company
                                                           380 HIDFVMSVKAKDDVYVDLIRFLREN 404
                                                                                                                                                                      Sequence 16, Application US/09073674 Patent No. 5998189 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CTISSEY, TOOR M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734,622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                               2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               734 622-1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS LENGTH: 380 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSE: Warner-La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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48105
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Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Ann Arbor
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                    US-09-073-674-16
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                                                                                                                                  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAVAMHL-------DQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Benlcourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
CORRESPONDENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>..</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 RFVPQSLFKFIFGDKIFYPHNFFDQFLAT-----
                                                                                                                                                                                                                                                                                    E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                            Sequence 16, Application US/08227108 Patent No. 5807726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 7620
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 antino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTOKNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
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Best Local Similarity 33.8
Matches 130; Conservative
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: New York
RY: U.S.A.
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                                                                                                                                                      GENERAL INFORMATION:
               371 SLMAKD 376
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                                                                                            US-08-227-108-16
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; MOLECULE TYPE: protein
US-09-073-674-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michigan
: U.S.A.
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EMISMMAED 377
                                                                                                                                   396 DLIRFLREN 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Ann Arbor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 48105
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280
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              323 RYGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYG 379
                               299 HYDQSQPPYYNVTAMNVPIAVW--NGGKDLLADPQDVGLLLPKL---PNLIYHKEIPFYN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 LPNNSLAFWLADAGYDVWLGNSRGNTWSRKNVYXSPDSVFFWAFSFDEMAKYDLPATINF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 VAMHLDQMLV--TMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENCCFNT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 VYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLRA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAAD-STGPPVFLQHGLFQGGDTWFIN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                                                                                                                                                                                                                                                  APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
AITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PACENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REGISTRATION NUMBER: 7620-033
TREECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                   380 HIDFVMSVKAKDDVYVDLIRFLREN 404
                                                                                                                                                                                                   Sequence 17, Application US/08227108 Patent No. 5807726
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 33.6
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
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TOPOLOGY: lin
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254 SRFDVYLGHNPAGTSVQDFLHWAQLVRSGKFQAFNWGSPSQNMLHYNQKTPPEYDVSAMT 313
                                                339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGHIDFVMSVKAKDDVYV 395
                                                                             : :| || || || || : :| : || : || || || 314 VPVAVW--NGGNDILADPQDVAMLLPKLSN---LLFHKEILAYNHLDFIWAMDAPQEVYN 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 VYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF-VLRA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 VAMHLDQMLV--TMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITG-ENCCFNT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAAD-STGPPVFLQHGLFQGGDTWFIN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09073674

Patent No. 5998189

GENERAL INFORMATION:
APPLICANT: Blanchard, Claine
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SURTHWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,674 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 534; DB 2; I
33.6%; Pred. No. 1.2e-49;
ive 73; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5072-D1-66-TMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAWE: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734,622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Warner-Lambert (STREET: 2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.6%
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA----- 218
                                                                                                               239 ALFIICGFDTMNLNMSRLDVYLSHNPAGTSVQNVLHWSQAVKSGKFQAFDWGSPVQNMMH 298
                 ----LDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN 265
                                                                                      266 LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR 323
                                                 -----EVCSRETVDLLCSN 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Dog Gastric Lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%; Score 529; DB 2; 32.5%; Pred. No. 4.4e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
TELECOMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
                                                 197 LVPSFLFKLIFGNKIFYPHHFFDQFLAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warner-Lambert Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/073,674 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09073674 Patent No. 5998189
                                                                                                                                                                                                                                                              354 LDFIWAMDAPQAVYNEIVSMM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Crissey, Todd M. REGISTRATION NUMBER: 37,807
                                                                                                                                                                                                                                       IDFVMSVKAKDDVYVDLIRFL 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 379 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
                 219 ---SFVLRAVAMH--
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                                                                                                                                                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSFDEMAKYDLPATID 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVYTVT-QSKILLYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA----- 218
198 IPTFLFKLMFGKKMFLPHTYFDDFLGTEV----CSREVLDLLCSNTLFIFCGFDKNLNV 253
                                                                          49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFI 106
                                                     SRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGLLG-NLRRYGHLRPPAFDLSSIP 338
                                                                                                                            339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGHIDFVMSVKAKDDVYV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 529; DB 1; 32.5%; Pred. No. 4.4e-49; tive 70; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REFERENCE/DOCKET NUMBER: 7620-033
TELECHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEFAX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08227108
Patent No. 5807726
GENEEL INFORMATION:
APPLICANT: Blanchard, Claire
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                     396 DLIRFLREN 404
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EMISMMAED 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124;
                                                                                                                                                                                                                                                                                             RESULT 6
US-08-227-108-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: N
STATE:
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Best Local 9
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Matches
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107 NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166
                      YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.4e-49;
); Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
CORRESPONDENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5072-D1-66-TMC
                                                                                                                             198 LVPSFLFKLIFGNKIFYPHHFFDQFLAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Warner-Lambert Company
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09073674
Patent No. 5998189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CTISSEY, TOGM M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEPHONE: 734 622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70;
                                                                                                                                                                                                                                                                                                                                       :||: :: | | | | :: : | | LDFIWAMDAPQAVYNEIVSMM 375
                                                                                                                                                                                                                                                                                                                381 IDFVMSVKAKDDVYVDLIRFL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Warner crreET: 2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 32.59
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLAND ZOUNTY: Ann Arbor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-073-674-5
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239 ALFIICGFDTMNLNMSRLDVYLSHNPAGTSVQNVLHWSQAVKSGKFQAFDWGSPVQNMMH 298
                                                                                 ----EVCSRETVDLLCSN 238
                                                                                                                           266 LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR 323
                                                                                                                                                                                                  YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGH 380
                                                                                                                                                                                                                        299 YHQSMPPYYNLTDMHVPIAVW--NGGNDLLADPHDVDLLLSKL---PNLIYHRKIPPYNH 353
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32.5%; Pred. No. 4.4e-49;
.ive 70; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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1155 Avenue of the Americas
                                                                                       197 LVPSFLFKLIFGNKIFYPHHFFDQFLAT----
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FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08227108
Patent No. 5807726
                                                                                                                                                                                                                                                                                               :11: :: | | | :: : : LDFIWAMDAPQAVYNEIVSMM 374
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 32.5
Matches 124; Conservative
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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STATE: New York
COUNTRY: U.S.A.
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Best Local Similarity 30.28 Matches 130; Conservative
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US-09-820-001-2
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Patent No. 6387680
GEMERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al
TITLE DE INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE DE INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOL186
CURRENT APPLICATION NUMBER: US/09/820,001
CURRENT PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                 138 FILKKTGODKLHYVGHSQGTTIGFIAFSTNPKLAKRIKTFYALAPVATVKYTETLLNKLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSAFLKWLGTHVCTHVILKELCG-NLCFLLCGFNERNLNMSRVDVYTTHSPAGTSVQNM
                                                                                                                                                                                                            ---SFVLRAVAMH-------LDQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN
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                                                                                         YVYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 392;
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                                                                                                                                                                                                                                                                    198 LVPSFLFKLIFGNKIFYPHHFFDQFLAT---
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TYPE: PRT
ORGANISM: Human
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US-09-820-001-4
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Sequence 2, Application US/09820001
Patent No. 6387680
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
THEREOF ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE OF INVENTION:
THEREOF ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE OF INVENTION:
THEREOF ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE REPERBACE: CL0001186
CURRENT APPLICATION NUMBER: US/09/820,001
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
SOFTWARR: FastsEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 AMHLDQMLVTMGIHQLNFRSDMGVQIVDS-LCDGE--HVDCNNLLSAITGEN-CCFNTSR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 LPIWMGYGGLDALADVTDVQRTIRELGSTPELLYIGDYGH--IDFVMSVKAKDDVYVDLI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LLLTTTCLICGTL-------NAGGFLDLENEVNPEVWMNTSEIIIYNGYPS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGYVYTVT-QSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 395;
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APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
350 DVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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30.2%; Pred. No. 4.5e-45;
iive 72; Mismatches 153
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Patent No. 5807726
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
    NUMBER OF SEQUENCES:
                                                                          Michigan
: U.S.A.
                                                              Ann Arbor
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                                                                         STATE: M
COUNTRY:
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Patent No. 5998189
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
1155 Avenue of the Americas
                                                                                                                                                                                                                     NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE-CACKET NUMBER: 7620-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                              APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               TELEFAX: 212 869-8864/9741
TELEEX: 66141 PENNIXE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 379 amino acids
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Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear / MOLECULE TYPE: protein US-08-227-108-18
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                           New York
: U.S.A.
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               New York
                                                       10036
                                                                                                                             SOFTWARE:
                           STATE: No COUNTRY:
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226 AMHLDQMLVTMG---IHQLNFRSDMGVQIVDSLCDGE--HVDCNNLLSAITG-ENCCFNT 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 ESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGHIDFVMSVKAKDDVYV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 VPIAVWS--GGNDWLADPQDVDLLLPKLSN---LIYHKEILPYNHLDFIWAMNAPQEVYN 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QLLLPLGYPCTEHNVETKDGFLLSLQHIPHG-KNKAADSTGPPVFLQHGLFQGGDTWFIN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 SAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 LPNNSLAFILADAGYGVWLGNSRGNTWSRRNLYYSPDSVEFWAFSFDEMAKYDLPATIDF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 VYTVT-QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASFVLRAV 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.4%; Score 491; DB 2; Length 379
31.7%; Pred. No. 6.2e-45;
tive 78; Mismatches 152; Indels
                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         5072-D1-66-TMC
  Company
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 6, Application US/09036987A; Patent No. 6143526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CT.15SEY, TOCH M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELECHONE: 734 622-7530
ADDRESSEE: Warner-Lambert STREET: 2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.78
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 734 622-1553
                                                                                                               ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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12;

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3-007-370-700-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 LLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTGPPV----FLQHGLFQGGDTWF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 INSAEQSLGYILAD-----NGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEY 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 ITGENCCFNTSRIDY-YLEYEPHPSSTKNLHHLFQMIRKGTFAKYDY----GLLGNLRRY 324
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                             APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Marlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Winner, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
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                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 ALPLILLVVSCCGRIVSGASPAA-----AALRRVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/036,987A
                      Crawford, Kathryn P.
Madduri, Krishnamurthy
Merlo, Donald J.
Treadway, Patti J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,479
Broughton, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
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Best Local Similarity 21.68
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2232 AVPL-----IVSGRTPAALSAQASALLSYLGERGDISTLDAAFSLASSRAALEER 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 INSAEQSLGYILAD-----NGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEY 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 LLPLGYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTGPPV----FLQHGLFQGGDTWF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 ITGENCCFNTSRIDY-YLEYEPHPSSTKNLHHLFQMIRKGTFAKYDY----GLLGNLRRY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 DLLAMLGYVYTVTQSKILYVGHSQGTIMGLAA----ĻTMPEIVKMISSAALLCPISYLDHV
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                                                     GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Rathryn P
APPLICANT: Treadway, Parti J
APPLICANT: Waldron, Clive
ITITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
ITITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
ITITLE OF INVENTION Blosynthetic Genes For Spinosyn Insecticide
ITITLE OF INVENTION Blosynthetic Genes For Spinosyn Insecticide
ENLERRY FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%; Score 105; DB 4; Length 5588; 21.6%; Pred. No. 0.75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-6
Sequence 6, Application US/09370700 Patent No. 6274350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 21.6% Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5588
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

December 30, 2002, 20:43:42; Search time 71 Seconds (without alignments) 99:983 Million cell updates/sec Run on:

US-09-699-652A-14 Title: Perfect score:

2194 1 MAMAGHAPGGALPLILLUVS......DDVYVDLIRFLRENGWHNSY 410 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

109717 segs, 17314136 residues Searched:

Total number of hits satisfying chosen parameters:

109717

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

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/cgn2\_6/ptodata/1/pubpaa/USO0\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 75, Appl	Sequence 2, Appli	Sequence 41, Appl		Sequence 4, Appli	Sequence 49, Appl	Sequence 2, Appli	Sequence 21, Appl	Sequence 47, Appl	Sequence 2, Appli	Sequence 50, Appl	Sequence 5, Appli	Sequence 52, Appl	Sequence 151, App	Sequence 567, App	7	Sequence 12337, A			
	DI	US-10-042-431-75	US-10-056-744B-2	US-10-042-431-41	2 US-10-003-302-4	0 US-09-811-825-4	US-10-042-431-49	0 US-09-811-825-2	0 US-09-835-996A-21	US-10-042-431-47	2 US-10-003-302-2	US-10-042-431-50	US-10-056-744B-5	US-10-042-431-52	0 US-09-923-779-151	0 US-09-925-297-567	0 US-09-778-927A-59	0 US-09-815-242-12337	0 US-09-944-807-10	0 US-09-950-368-6	
	Query Match Length DB	398	398 9	399 9	392	374 I	390	398	409 1	423 9	395 1	221 9	127 9	144 9	465 1	473 1	1602 1	305 1	972 1	298 1	
æ	Query Match 1	24.9	24.2	23.5	23.1	22.9	22.9	22.9	22.9	22.9	22.4	17.5	12.0	5.5	4.1	4.1	4.1	. 4.1	4.0	4.0	
	Score	546	531	515.5	507.5	502	502	502	502	502	492.5	384.5	264	114.5	90.5	90.5	90	88	88	87.5	
	Result No.	1	7	m	4	2	9	7	60	6	10	11	12	13	14	15	16	17	18	19	

NSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLG 166 

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Sequence 58, Appli Sequence 7, Appli Sequence 4, Appli Sequence 25, Appli Sequence 25, Appli Sequence 947, Appli Sequence 947, Appli Sequence 14, Appli Sequence 13513, Aspli Sequence 1, Appli Sequence 4, Appli Sequence 23, Appli	HAVING DIAGNOSTIC, OTHER USES	Length 398; ; 2; Indels 52; Gaps 13; -PPVFLQHGLFQGGDTWFI 106	
10 US-09-778-927A-58 12 US-10-080-644-7 9 US-10-11-736-4 10 US-09-895-578-4 9 US-09-895-793-947 10 US-09-895-793-947 10 US-09-895-793-14 10 US-09-895-793-14 10 US-09-815-242-13513 9 US-09-815-242-13513 10 US-09-811-239-3 10 US-09-811-239-3 10 US-09-811-239-1 10 US-09-955-29 10 US-09-955-45 10 US-09-929-955-45 10 US-09-929-955-47 10 US-09-929-955-47 10 US-09-929-955-48	ALIGNMENTS 042431 1 1 er C Es ENCODING PROTEINS VE, THERAPEUTIC, AND 5/10/042,431 -25 09/333,159 09/578,063	b; Score 546; DB 9; b; Pred. No. 2.1e-44 70; Mismatches 13 71LSLQHIPHGKNKAADSTG-	α
20 87.5 4.0 1251 22 85.5 3.9 2799 24 85.5 3.9 2799 25 84.5 3.9 2799 26 83.5 3.9 2799 27 84.5 3.9 2799 28 83.5 3.9 2799 29 83.5 3.9 669 30 82.5 3.8 676 31 82 3.7 728 32 82 3.7 728 33 82 3.7 686 34 81 3.7 686 36 81 3.7 686 37 81 3.7 686 38 81 3.7 686 39 81 3.7 686 40 81 3.7 686 41 81 3.7 686 42 81 3.7 686 43 81 3.7 686 44 81 3.7 686 45 86 81 3.7 686 46 81 3.7 686 47 81 3.7 686 48 81 3.7 686 49 81 3.7 686 40 81 3.7 686 41 81 3.7 686 42 81 3.7 686 43 81 3.7 686 44 81 3.7 686	RESULT 1  US-10-042-431-75  Sequence 75, Application US/10042  Publication No. US2020182675A1  GENERAL INFORMATION: APPLICANT: MCCARTHY, Sean A  APPLICANT: BRANES, Thomas M  APPLICANT: FRASER, Christopher of the control of the cont	Ouery Match 24.99 Best Local Similarity 33.99 Matches 130; Conservative Oy 49 QLLLPLGYPCTEHNVETKDGI	37

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US-10-042-431-41
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US-10-003-302-4
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                                                                                                                                            59 TEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFINSAEQSLGYI 116
-------DQMLVTMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNN 265
                                                              26 LLSAITG-ENCCFNTSRIDYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRR 323
                                                                                324 YGHLRPPAFDLSSIPESLPIWMGYGGLDALADVTDVQRTIRELGSTPELLY---IGDYGH 380
                               -- EVCSREMLNLLCSN 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 AMHLDQMLVTMGIHQLNFRSDMGVQIVDS-LCDGE--HVDCNNLLSAITGEN-CCFNTSR
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                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10056744B

Publication No. US200201933031

GENERAL INFORMATION:
APPLICANT KAPELLET-LIBERMANN, ROSANA

TITLE OF INVENTION: 58860, A HUMAN CHOLESTERYL

TITLE OF INVENTION: HYDROLASE AND USES THEREFOR

TITLE OF INVENTION: HYDROLASE AND USES THEREFOR

FILE REFERENCE: MPI2001-026PIRM

CURRENT APPLICATION NUMBER: US/10/056,744B

CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: 60/264,167

PRIOR PILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PRASESEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 398
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                                216 FVPQSLFKFIFGDKIFYPHNFFDQFLAT --
                                                                                                                                                                                       381 IDFVMSVKAKDDVYVDLIRFLREN 404
                                                                                                                                                                                                                   LDFIWAMDAPQEVYNDIVSMISED 396
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ORGANISM:
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Sequence 4, Application US/10003302

Patent No. US/200201435A1

GREEAL INFORMATION:
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/003,302
CURRENT FILING DATE: 2001-12-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GPVA----SVAFCTSPMAKLGRLPDHL-------IKDLFGDKEFL 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 GSGGL------CDQLLLPLGYPCTEHNVETKDGFLLSLQHIPHG-KNKAADSTGP 89
                                                                                              APPLICANT: BARNES, Thomas M
APPLICANT: BARNES, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: OVOEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-6U2
CURRENT APPLICATION NUMBER: US/10/42,431
CURRENT FILING DATE: 2000-10-25
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 DWSWQELAEYDLLAMLGYVYTVT-QSKILYVGHSQGTIMGLAALT-MPEIVKMISSAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 -----GEHVDCNNLLSAITGENCCF-----NTSRIDYYLEYEPHPSSTKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 CPISYLDHVSASFVLRAVAM-----HLDQMLVTMGIHQLNFRSDMGVQIVDSLCD----
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Sequence 41, Application US/10042431 Publication No. US20020182675A1
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                                                     GENERAL INFORMATION: APPLICANT: MCCARTHY,
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APPLICANT: MCCARRHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: BARNES, Thomas M
APPLICANT: FASER, CHIStopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEC ID NOS: 79
SOFTWARE: PATENTI VET. 2.1
                                                                                                182 -LPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGGFNTNNNNMSRA 240
                                                                                                                                                                                                                                              198 -LPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGGFNTNNMNMSRA 256
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   173 -OSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA---SFVLRAVAM 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 GQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKMYFALAPIATVKHAKSPGTKFLL---- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                        SVYAAHTLAGTSVQNILHWSQAVNSGELRAFDWGSETKNLEKCNQPTPVRYRVRDM--TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 -QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA---SFVLRAVAM
                                                                         228 HLDQMLV--TMGIHQLNFRSDMGVQIVDSLCDGEHVD--CNNLLSAITGENC-CFNTSRI
                                                                                                                                                 DYYLEYEPHPSSTKNLHHLFQMIRKGTFAKYDYGL-LGNLRRYGHLRPPAFDLSSIPESL
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34.0%; Pred. No. 3.3e-40;
live 67; Mismatches 146;
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Matches 124; Conservative
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APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MULECULES ENCODING HUMAN LIPASE PROTEINS, AND UTITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOLING

CURRENT APPLICATION NUMBER: US/09/811,825

CURRENT FILING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                        90 PVFLQHGLFQGGDTWFINSAEQSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFW 149
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                                                                                                                                            23.1%; Score 507.5; DB 12;
llarity 32.4%; Pred. No. 1e-40;
Conservative 57; Mismatches 141;
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Patent No. US20020144297A1
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                                                                                       ORGANISM: Homo sapiens
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Matches 130; Conserv
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ORGANISM: Human
                                                   LENGTH: 392
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APPLICANT: Wind, Dunrul
APPLICANT: Wind, Dunrul
APPLICANT: Wind, Dunrul
TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
FILE REFERENCE: 28110/35915A
CURRENT APPLICATION NUMBER: US 60/197,137
PRIOR PLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/714,936
PRIOR FILING DATE: 2000-011-17
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR APPLICATION NUMBER: US 09/667,298
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR APPLICATION NUMBER: US 09/631,451
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: DDM
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Publication No. US20020182675A1
GENERAL INFORMATION:
APPLICANT: MCCARTHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
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Zhao, Qing
Wehrman, Tom
Drmanac, Radoje
                                                                      Ren, Feiyan
Qian, Xiahong
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US-09-835-996A-21
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANY: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1170
CURRENT APPLICATION NUMBER: US/09/811,825
CURRENT FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 2.
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315 PTAMWIGGODWLSNPEDVKMLLSEV---TNLIYHKNIPEWAHVDFIWGLDAPHRMYNEII 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 GYPCEEYEVATEDGYILSVNRIPRGLVQ-PKKTGSRPVVLLQHGLVGGASNWISNLPNNS 90
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Patent No. US20020142953A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis
APPLICANT: Loeb, Debra
APPLICANT: Toob, Debra
APPLICANT: Toob, Ping
APPLICANT: Too, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                            Sequence 2, Application US/09811825 Patent No. US20020144297A1
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; ORGANISM: Human
US-09-811-825-2
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                                                    399 RFLRE 403
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US-09-811-825-2
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; Sequence 50, Application US/10042431; Publication No. US20020182675A1; GENERAL INFORMATION:
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      4 LLLTTTCLICGTL----
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Matches 78; Conserv
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Patent No. US200201424351
Patent No. US200201424351
APPLICANT: WERKULOV, Gennady et al.
APPLICANT: WERKULOV, Gennady et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001186DIV
CURRENT APPLICATION NUMBER: US/10/003,302
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fat-SEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 -LPDMMIKGLECKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGGFNTNNMNMSRA 289
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                                                                                                                                                                                                                                                                                                    55 GYPCTEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFINSAEQS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                   173 -QSKILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSA---SFVLRAVAM 227
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                                                                                                                                                                                                                                     22.9%; Score 502; DB 9; Length 423; 34.0%; Pred. No. 3.7e-40;
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                                                                                                                                                                                                                                                                  67; Mismatches 146; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 ILLVVSC--CGRIVSGASPAAAALRRVGSGSGGLCD---
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/33,159
PRIOR FILING DATE: 1999-06-14
PRIOR PELING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO47
LENGTH: 423
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                                                                                                                                                                                 ORGANISM: Homo sapiens
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US-10-003-302-2
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APPLICANT: MCGARFHY, Sean A
APPLICANT: BARNES, Thomas M
APPLICANT: BARNES, Thomas M
APPLICANT: BARNES, Thomas M
APPLICANT: FARSER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
CURRENT APPLICATION NUMBER: US/10/042,431
CURRENT FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN VET. 2.1
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                                                   59 TEHNVETKDGFLLSLQHIPHGKNKAADSTG--PPVFLQHGLFQGGDTWFINSAEQSLGYI 116
                                                                                  LADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEYDLLAMLGYVYTVT-QSK 175
                                                                                                                                                                                                                                                                       ILYVGHSQGTIMGLAAL-TMPEIVKMISSAALLCPISYLDHVSASF------VLRAV 225
                                                                                                                                                                                                                                                                                                                                                                                AMHLDQMLVTMGIHQLNFRSDMGVQIVDS-LCDGE--HVDCNNLLSAITGEN-CCFNTSR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 LPIWMGYGGLDALADVTDVQRTIRELGSTPELLYIGDYGH--IDFVMSVKAKDDVYVDLI 398
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-- NAGGFLDLENEVNPEVWMNTSEIIIYNGYPS 47
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394 YVDLIRFLRE 403
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121 YNEIIHLMQQ 130
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US-09-923-779-151
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Sequence 52, Application US/10042431
Sequence 52, Application No. US20020182675A1
SEQUENCE 52, Application No. US20020182675A1
SERENAL INFORMATION:
APPLICANT: MCCARTHY, Sean A
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-602
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                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                                           Sequence 5, Application US/10056744B
FUBLICATION NO. US20020193303A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: HYDROLAGE AND USES THEREFOR
FILE REFERENCE: MPIZOO1-026P1RNM
CURRENT APPLICATION NUMBER: US/10/056,744B
FRICK APPLICATION NUMBER: 60/264,167
PRIOR FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.2%; Score 114.5; DB 9;
24.6%; Pred. No. 0.00089;
live 30; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 264; DB 9;
44.2%; Pred. No. 3.9e-18;
tive 18; Mismatches 47
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR PLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52
LENGTH: 144
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    : Homo sapiens
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Best Local Similarity
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; 'ORGANISM: HOM
US-10-056-744B-5
                             US-10-056-744B-5
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Best Local S:
Matches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 FINSAE----QSLGYILADNGFDVWIGNVRGTRWSKGHSTFSVHDKLFWDWSWQELAEY 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 LANVCKNLFKVESVNCICVD-----WKGGSR-----TGYTQASQNIRIV----GAEVAYF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 DLLAMLGYVYTVTQSKILYVGHS------QGTIMGLAALT-----MPEIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 RLDPSDAKFVDVIHTDGAPIVPNLGFGMSQVVGHLD-FFPNGGVEMPGCKKNILSQIVD- 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 LCDG-----EHVDCNNLLS-----AITGENC------CF----NTSR 281
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Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

FILE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPREBRICE: PA105

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12
                                                        GENERAL INFORMATION:
APPLICANT: Pyle, Ruth A.
APPLICANT: Pyle, Ruth A.
APPLICANT: Ruth, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/09/923,779
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 151, Application US/09923779
; Patent No. US20020076721A1
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4.1%; Score 90.5; DB 10; Length 473;
Best Local Similarity 20.4%; Pred. No. 0.91;
Matches 80; Conservative 55; Mismatches 146; Indels 111; Gaps
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 567
LENGTH: 473
                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Listing first 45 summaries

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HSLAL AK091558 AX477670

AX091558 Homo sapi AX477670 Sequence L26319 Bos taurus

AX392821 Sequence

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M74775 Human lysos BC012287 Homo sapi X76488 H.sapiens m

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SUMMARIES

DB

Length

Match Query

JO8464 Human lysos

331690 H.sapiens

HSU08464 HSLYACLY HUMLIPCHL BC012287

2481 2481 2493 2586 2626 2982 1272

AX472752 Sequence AC004766 Drosophil AC008342 Drosophil AC017903 Drosophil

93932 175007 211784

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ALIGNMENTS

AX392824 Sequence S81497 lysosomal

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AE003783 Drosophil AC018484 Drosophil AC017119 Drosophil

DMLIPASE3 AC013100 AC013100 AC008360 AC008360 AC01569 AC017119 AC017119 AC01783 AC018484 AC018484 AC018484 AC018484 AC018484

82393 194672

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AC006298 57564 bp DNA linear PLN 27-FEB-2002 Arabidopsis thaliana chromosome 2 clone F15A23 map mi398, complete Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida; Eurosidae; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 57564)
Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E., AC006298 AC006298.13 GI:20197742 Arabidopsis thaliana. Arabidopsis thaliana AC006298 sedneuce VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

Pred. No. is the number of results predicted by chance to have a

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COMPLEMENT (501): 7730)
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                                                                                                                      Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA (bases 1 to 57564) Town, C.D. and Kaul,S. Direct Submission Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org on Apr 18, 2002 this sequence version replaced gi:6598553.
Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M.,
Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D.,
Nierman,W.C., Fraser,C.M. and Venter,J.C.
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3078. 3173,3541. 3609,3810. 3868,3974. 4096,4191.
4352. 48815)
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(AC007267:4979. .55686)."

446. .4815

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Chaeses to 793)

Koesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Ouach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R. Direct Submission

Submitted (09-JUL-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, Biological Studies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLSPVAYLSHMTTVIGDIAAKTFLAEATSILGWPEFNPKSGLVG
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QFKYHDIDKMNYQFYRDYAHAPFINGVYAROVYNQVATFFRRQA
AY048236 793 bp mRNA linear PLN 05-AUG-2001
Arabidopsis thaliana AT5g14180/MUA22_18 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Koesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J. M., Goldsmith, A.D., Jiang, P. X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Nguyen, M., Ondera, C.S., Palin, C.J., Pham, P.K., Quech, H.L., Southwick, A., Davis, R.W., Theologis, A., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collection and clustering of RAFL cDNAS (RAFL CDNA: 'RIKEN ATABLADOSIS Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Roesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Gibson, H.A., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Falm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinozaki, K., Davis, R., Theologis, A. and Ecker, J.R.
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llarity 63.0%; Pred. No. 2.1e-19;
Conservative 0; Mismatches 124;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                         Gaps
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                                                                                                                                                      AGAGCAGTCGCCATCTTGATCAGATGCTTGTTACTATGGGAATTCACCAGCTGAAC
                                                                                                                                                                                                                                                          818 TGCAACAATTTGCTATCTGCGATTACAGGGGAAAACTGTTGCTTCAATACATCAAGGATT
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 Length 793;
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 DB 8;
6.8%; Score 100.8; DB 8;
48.9%; Pred. No. 8.1e-12;
iive 0; Mismatches 342;
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Direct Submission
Submitted (08-APR-1994) Hong Du, Division of Human Gentics,
Children's Hospital Medical Center, 3333 Bernet Street, Cincinnati,
OH 45229-3039, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                         166 GGATTCCCTAGTGAGGAATACCTAGTTGAGACAGAAGAAGATATATTCTGTGCCTTAAC 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                               371 GGGTATATCCTTGCTGATAACGCTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 CAAGAGTTAGCTGAATATGACCTTTTAG---CAATGCTAGGCTATGTGTATACAGTCACA 547
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                                                                                                                                         Length 2481;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2481)
Du,H. and Gregory,G.A.
                                         /note="EMBL/GenBank Accession No. 231690"
477 c 513 g 799 t
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                                                                                                                                                                                     Indels
                                                                                                                                    Score 94.2; DB 6;
Pred. No. 2.9e-10;
0; Mismatches 193;
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/db_xref="taxon:9606"
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/organism="Homo sapiens'
/db_xref="taxon:9606"
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/cell_line="hepg2"
/cell_type="hepatoma"
                                                                                                                                      6.48;
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                                                                                                                                                            Best Local Similarity 55.2
Matches 249; Conservative
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GFPSEEYLVETEDGYILCLNRIPHGRKNHSDKGPKPVVFLQHGLLADSSNWVTNLANS
SLGFILLADAGFDVWMGNSRCNTWSRKHKTLSVSQDEFWAFSYDEMAKYDLPASINFIL
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LEPHLIKDEGDKEFLDGSAFLKWLGTHYVCTHYLKELCGULCFLLCGFNENLINMSR
VDYYTTHSPAGTSVONMLHWSQAVKPQKPDMGSSAKNYFHYNGSYPPTYWKDML
VPTAVWSGGHDWLADVYDVNILLITQITNLVFHSSIPEWBHLDFIWGLDAPWRLYNKIL
                                                                                     Putative Functional Motifs between Mouse
                                                                                                                                                                    Direct Submission
Submitted (O5-APR-1994) Hong Du, Division of Human Genetics,
Children's Hospital Medical Center, 3333 Bernet Street, Cincinnati,
OH, 45229-3039, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKMRFLGLVVCLVLWTLHSEGSRGKLTAVDPETNMNVSEIISYW
                      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                         ib="human liver HepG2 cDNA library/lambda 2AP"
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Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2481)
Du,H. and Gregory,G.A.
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Pred. No. 2.9e-10;
); Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="lysosomal acid lipase"
/protein_id="ch83495.1"
/db_xref="G1:506431"
/db_xref="SPTREMBL:Q16529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="lysosomal acid lipase"
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/organism="Homo sapiens"
                                                                             Structural Conservation of Putal and Human Lysosomal Acid Lipase Unpublished
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                        /clone="clone hLAL"
/cell_type="hepatoma"
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /tissue_type="liver
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/citation=[1]
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/gene="LAL"
97. .1230
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ilarity 55.2%;
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2459. .2464
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AUTHORS
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                                                                                    TITLE
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LPHLIKDLEGDKEFLPQSAFLKWLGTHVOTHVILKELCGNLCFLLCGFUERNLNMSR
VDVTTHSPAGTSVQNMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDML
VPTAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIMGLDAPWRLYNKII
NLMRKYQ"
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SLGFILADAGFDVWMGNSRCNTWSRKHKTLSVSQDEFWAFSYDEMAKYDLPASINFIL
                                                                                                                   /translation="MKMRFLGLVVCLVLWTLHSEGSRGKLTAVDPETNMNVSEIISYW
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231690
 /clone_lib="HepG2 cDNA library/Lambda 2AP"
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ilarity 55.2%; Pred. No. 2.9e-10;
Conservative 0; Mismatches 193;
                                                                                                                                                                                                                                                                          /product="lysosomal acid lipase"
79
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Homo sapiens.
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                                                                                  /protein_id="AAB60328.1"
/db_xref="G1:505053"
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                                                  /codon_start=1
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1234. .2480
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Matches 249; Conserv
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COUNT 69:
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/protein_id="AAA5919.1"
/db_xref="GI:187152"
/db_xref="GDB:00-120-153"
/translation="MKMRFLGLVVCLVLWPLHSEGSGGKLTAVDPETNMNVSEIISYW
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SLGFILADAGFDVWMGNSRGNTWSRKHKTLSVSQDEEWAFSYDEMAKYDLPASINFIL
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VDVYTTHSPAGTSVONMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDML
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human lysosomal acid lipase/cholesteryl esterase mRNA, complete
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Anderson, R.A. and Sando, G.N.
Cloning and expression of cDNA encoding human lysosomal acid
lipase/cholesteryl ester hydrolase. Similarities to gastric and
                                              547
                                                                                                                                                                           466 GATGAGATGGCAAAATATGACCTACCAGCTTCCATTAACTTCTGAATAAAACTGGC 525
286 CAACATGGCTTGCTGGCAGATTCTAGTAACTGGGTCACAAACCTTGCCAACAGCAGCCTG 345
                                                                                            TGGAGTAAAGGTCATTCAAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
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                                                                                                                                                                                                                                           /note="alternate initiator ATG may be at position 47"
                                                                                                                                                          CAAGAGTTAGCTGAATATGACCTTTTAG ---CAATGCTAGGCTATGTGTATACAGTCACA
                                GGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGT
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J. Blol. Chem. 266 (33), 22479-22484 (1991)
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/db_xref="taxon:9606"
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/EC_number="3.1.1.13"
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/note="G00-120-153"
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/note="alternate signal peptide may begin at position 47; as predicted from von Heljne, G. (1986) Nucl. Acids Res. 14,4683-4699; G00-120-153"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2586)
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Submitted (06-400-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                        /product="lysosomal acid lipase/cholesteryl esterase"
/EC_number="3.1.1.13"
/note="G00-120-153"
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                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Similar to lipase A, lysosomal acid, cholesterol seterase (Wolman disease)"
/protein_id="Aah12287.1"
/db_xxef="G1.15126727"
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                                                                                                                                                                                                                                                                                                                        found
                                                                                                                                                                   Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 3 Row: c Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 434305. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 GGCTACCCCTGCACCACGACGTTGAAACAAAGATGGATTCCTTTATCTCTTCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 GGATTCCCTAGTGAGGAATACCTAGTTGAGACAGAAGATGGATATATTCTGTGCCTTAAC 292
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                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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Pred. No. 2.9e-10;
0; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity 55.2%;
Matches 249; Conservative
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NKTGOEQVYYVGHSQGTTIGFIAFSQIPELAKRIKMFFALGPVASVAFCTSPMAKLGR
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VDVYTTHSPAGTSVQNMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDML
VPTAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKII
                                                                                                                                                                                                                                                                                                                                                PRI 25-FEB-1994
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (29-NOV-1993) D. Ameis, Medical Department, University
Hospital Eppendorf, Martinistrasse 52, 20246 Hamburg, FRG
Location/Qualifiers
   607
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                                   548 CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTTTGGCGGCTTTG
                                                                                                                                                                                                                                                                                                                                                linear
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H.sapiens mRNA for lysosomal acid lipase.
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AX477670.1 GI:22216841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK091558 2982 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ34239 fis, clone FCBBF3027755, highly similar to LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                          CATATCCCACATGGCAAAATAAAGCAGCAGATAGTACTGGCCCTCCAGTT---TTTCTT 310
                                                                                                                                                                                                               CAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTGAGCAATCACTT 370
                                                                                                                                                                                                                                                                                                                                                     TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
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                                                                     GCCTACCCCTGCACCAGCACCATGAAACAAAAGATGGATTCCTTTTATCTTCAG 253
                                                                                          CAACATGGCTTGCTGGCAGATTCTAGTAACTGGGTCACAAACCTTGCCAACAGCAGCCTG 457
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                                      Gaps
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF3
   Length 2626;
                                    193;
Score 94.2; DB 9;
Pred. No. 2.9e-10;
0; Mismatches 193;
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AK091558
AK091558.1 GI:21749961
Query Match 6.4%;
Best Local Similarity 55.2%;
Matches 249; Conservative
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Homo sapiens
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TITLE
JOURNAL
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construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- 6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Glitzach,K.J., Sapperstein,S.K., Honchell,C.D., Bruns,C.M.,
Duggan,B.M., Xu.Y. and Lee,S.
Lipid-associated molecules
Patent: WO 02464184 8 13-JUN-2002;
Incyte Genomics, Inc. (48)
Location/Qualifiers
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Pred. No. 6.8e-10;
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Mammalia; Eutheria; Primates; Catarrhini
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                                                                                                                                                                                             /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="FCBBF3027755"
/tissue_type="brain"
/clone_lib="FCBBF3"
/dev_stage="fetal"
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Sequence 8 from Patent WO0246418.
AX477670
                                                                                                                                                                                                                                                                                                                                                                            /note="cloning vector:
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\(\text{LD2002}\) mRNA linear ROD 07-AUG-2002 \) MUS musculus, RIKEN CDNA 4632427C23 gene, clone MGC:25790 \) IMAGE:4020396, mRNA, complete cds. \(\text{BC031933}\)
           /db_xref="01:600757"
//db_xref="01:600757"
//translation="MWMLLVTVCFIHMSGNAFCFLGKIAKNPEASMNVSQMISYWGYP
//translation="MWMLLVTVCFIHMSGNAFCFLGKIAKNPEASMNVSQMISYWGYP
SEMHKVTTANGYILQYYRIPHGKNNTANHLGQRFVYFLQHGLGSATNNTISNLFKNSLG
FLLADAGYDVMLGNSRGNTWAQEHLYYSPSPFLARFIKNFALFRF
GQKKLHTVGHSQGTTTGFIARSTSPTLARFIKNFYALAPVAYVKYTKSLFNKLALIPH
FLFKIIFGDKMFYPHTFLEQFLGVEMCSRETLDVLCKNALFAITGVDNKNFNMSRLDV
                                                                                                           Y IAHNPAGTSVONTLHWRQAVKSGKEQAFDWGAPYQNLMHYHOPTPPIYNLTAMNVPI
AVWSADNDLLADPQDVDFILSKLSNLIYHKEIPNYNHLDFIWAMDAPQEVYNEIVSLM
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Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTTTATCTTCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                       496 GATGABAATGGCGGAATATGACTTCATCTTAAGGAGAAACAGGA
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                                                                                                                                                                                                                         /function="triacylglycerol acylhydrolase"
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                                                                                                                                                                                                                                                                                                                                    Score 88; DB 4;
Pred. No. 6.2e-09
                                                                                                                                                                                       /product="pregastric esterase"
/EC_number="3.1.1.3"
                                                                                                                                                                                                                                                                                        427
/protein_id="AAA57037.1"
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1378. .1385
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polyA_site
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mat_peptide
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1 (bases 1 to 1417)
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                                                                                                          Length 1272;
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The CDNA sequence encoding bovine pregastric esterase
65011625 (2), 259-262 (1994)
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Bos taurus pregastric esterase mRNA, complete cds.
L26319
                                                                                                                                       Indels
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Bos taurus 25 weeks Tongue serous gland cDNA
Bos taurus
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                                                                                                                                      196;
         /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte_ID No: 7483978CB1"
263 c 311 9 347 t
                                                                                                           DB 6;
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/cell_type="Secretory cell"
/tissue_type="Tongue serous g
/dev_stage="25 weeks"
73. .1266
/EC_number="3.1.1.3"
                                                                                                        6.0%; Score 89.4; DB
llarity 53.6%; Pred. No. 3e-09;
Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSEILSRVWTVSHRVEIWLLILVAYLLQRNVNSGHLPTKAADPE
AFMNVSEIIKHKGYPSEEYEVATEDGYILSVNRIPRGQTRLKKEGSRPVVLLQHGLLG
DASNWISNLPNNSLGFILADAGFDVWMGNSRGNTWSRKHKTLSIDQDEFWAFSYDEMA
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KYARSPGTKFLLLPDMHIKVLFGROBFLYQTRFFROLFIYLCGQMILDQICSNIILL
GORININMINNSRANVYVAHTPAGTSVQNILHWSQAVNSGELRAFDWGSETKNOEKCNQ
PTPIRXKVRDMMYPFAMTGQDMLSNPDDVKTLLSEVTNLIYHKNIPEWAHVDFIWG
LDAPQRYYNEIIHLMKQEPNLPQGTCRVKL"
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
                    3ene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                     Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M. Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MGC:25790 IMAGE:4020396"
/tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wht1 model. Expression driven by an MMTV-LTR
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0; Mismatches 190; Indels
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/protein_id="AAH31933.1"
/db_xref="G1:21594466"
                                                                                                                                                                                                                                   Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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/lab_host="DH108"
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Best Local Similarity 53.8%;
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AY091711 618 bp mRNA linear PLN 13-APR-2002
Arabidopsis thaliana AT5g14180/MUA22_18 mRNA, complete cds.
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Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Chan, M.M.,
Chang, E., Dale, J. M., Deng, J. M., Goldsmith, A.D., Jones, T.,
Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Miranda, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W.,
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Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
Bowser, L., Land, B., Lee, J.M., Lin, J., Miranda, M., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Tanada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
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                                                                                                                                                                                                                                                                                    CAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCTATGTGT----ATACAGTCACA
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FEATURES

CDS

ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             194 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAGATGGATTCCTTTTATCTTTCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 CATATCCCACATGGCAAAATAAAGCAGCAGATAGTACTGGCCCTCCAGTT---TTTCTT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTTTGGCGCTTTG 607
                                                                                           Griffin,J.A., Patterson,C., Gandhi,A.R., Lu,Y., Yao,M.G., Baughn,M.R., Walla,N.K., Hafalla,A.J., Ding,L., Tribouley,C..Das,D., Thornton,M. and Lal,P.
Lipid metabolism enzymes
Patent: WO 0216597-A 7 28-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBRG44C02 41805 bp DNA linear INV (
Caenorhabditis briggsae cosmid G44C02, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                 Length 1228;
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                                                                                                                                                                                                                        1. .1228
/organism="Homo sapiens"
/db_xref="taxon:9666"
/note="Incyte ID No: 7479063CB1"
^a44 c 259 g 349 t
                                                                                                                                                                                                                                                                                                                                                                 Score 86.4; DB 6;
Pred. No. 1.4e-08;
0; Mismatches 191;
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    Location/Qualifiers
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Caenorhabditis briggsae
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Best Local Similarity 53.5%;
Matches 227; Conservative (
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Wilson, R.
                       Homo sapiens
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KELRKIVKGSSDRNIKHYGQAIPPAVISAIPHELPLFFSYGGLDSLADVKDVEFLLD
QFKYHDIDKNNYQKDYAHDFINGYTAKDVVYNQVATFFKRQA"
144 c 130 g 169 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1071 ATGGAGGTCTTGATGCATTGGCTGATGTAACCGATGTTCAGCGTACTATCAGAGAGCTGG 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TCCTCGCCGAGGCCACCTCTATTCTTGGATGGCCAGAGTTTAACCCGAAAAGTGGATTAG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 TAGGGGATTTTATAAAGGCTATATGCCTTAAAGCGGGGATCGACTGTTATGATTTAGTCT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCTATTTCTTATCTTGATCATGTTAGTGCTAGTTTTGTTCTCAGAGCAGTCGCCATGC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                   5.8%; Score 86.6; DB 8; Length 518;
49.7%; Pred. No. 1.1e-08;
tive 0; Mismatches 274; Indels 1
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                                 /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                 51
                                                                                                                                                                                                          /product-"AT5914180/MUA22_18"
/protein_id="AAM10310.1"
/db_xref="GI:20147187"
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                                                                                           /clone="U13071"
/note="This clone is in pUNI
ecotype: Columbia"
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                                                                                                                                                                       /note="unknown protein"
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Sequence 7 from Patent W00216597,
AX392821 AX392821.1 GI:19700917
Location/Qualifiers
                                                                           /chromosome="5"
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Direct Submission
Submitted (04-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
Submitted by:
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                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

Location/Qualifiers
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Department of Genetics, Washington University,
St. Louis, MO 63110, USA
e-mail: jspieth@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 41805;
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Pred. No. 3.6e-08;
0; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis briggsae"
/strain="GujArat G16"
/db_xref="taxon:6238"
The sequence of C. briggsae cosmid G44C02 Unpublished
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Job time : 3950 secs
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8049 c 81
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Waterston, R.
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Matches, 193; Conservative
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Human TANGO 294 OR Human CG162 (or C5 Human CG162 (or C5 Human TANGO 294 CD

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Human secreted exp

Human lysosomal ac Human stomach cell Sequence encoding
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Scoring table:

Searched:

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Human lysosomal ac Nucleotide sequenc Canine gastric lip

Human breast cance

Drosophila melanog

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Triacylglycerol lipase; rice; fatty acid; seed oil; vegetable oil; transgenic plant; ss.
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AAN50385
ABL06473
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ABK12385
AAH50931
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AAZ34952
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ABK12388
AAD31193
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AAD27802
AAH78205
AAL24482
AAQ68388
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ABL29771
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Oryza sativa
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AAZ34956
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Human shear stress
Kid goat pregastri
Yeast YE-1 express
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Soybean acid triac
Soybean acid triac
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                                                                       (without alignments)
11885.101 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqn-emb1/Na1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/Na1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/Na1981.DAT:*
/SIDS2/gcgdata/geneseqn-emb1/Na1983.DAT:*
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                                                             December 30, 2002, 17:10:06; Search time 281 Seconds
                                                                                                                                                                                       4370478
       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                     Total number of hits satisfying chosen parameters
                                                                                                                                                                   2185239 seqs, 1125999159 residues
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Listing first 45 summaries
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AAZ34959
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AAI97406
ABN97383
AAH02906
ABL57144
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Gapop 10.0 , Gapext 1.0
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1483 445.6 184.6 94.2 94.2 94.2 91.2

Score

Result . Ю

Dog gastric lipase Canine gastric lip Human lysosomal ac Human protein HP03 Human triacylglyce

AAY32307

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This is the nucleotide sequence of the CDNA insert in clone

rir72.pk0015.b2 encoding the entire rice acid triacylglycerol
lipase (TAGL) (see AAY23207). The clone was isolated from a rice
lapse (TAGL) (see AAY23207). The clone was isolated from a rice
lapse (TAGL) see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,

cate a prepared recombinantly and used to raise antibodies, which
are used for detecting the enzymes in situ in cells or in vitro in
cell extracts. The polynucleotides may be used to create transgenic
plants in which the TAGL levels are present at higher or lower levels
than normal, or in cell types or developmental processes where they are
not normally found. This would alter the level of triacylglycerol and
cholesteryl esters found in those cells. Accumulation of fatty acids
with unusual structures may be a positive phenotype in plants used for
foods. In addition, it may be desirable to eliminate expression of TAGL
genes for certain applications. TAGL enzymes may also be used of olis, the TAGL enzymes can also be used as targets to facilitate the
design and/or identification of inhibitors of those enzymes that may be
useful as herbicides. This is desirable because inhibition of plant
cells the polynucleotides also serve as a source of probes and
cell private the contains and to inhibitory of enters.

Correct the polynucleotides also serve as a source of probes or the correct of property.
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linked to those genes, and to isolate homologous sequences from other
          the
          to alter
plant triacylglycerol lipase polynucleotides used of the enzyme in transgenic plants \,
                                                                                                                                                          65pp; English.
                                                                                                                                                          Claim 2; Page 44;
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Sequence 1483 BP; 375 A; 334 C; 344 G; 430 T; 0 other;

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 DB 21; Length 1483;
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; Score 1483; D
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0; Mismatches
100.0%;
           Best Local Similarity 100.
Matches 1483; Conservative
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AA234953 standard; cDNA; 859

RESULT 2 AAZ34953

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                        TICITATCTTGATCATGTTAGTGCTAGTTTTGTTCTCAGAGCAGTCGCCATGCATCTTGA
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                                                 GGCTTTGACGATGCCCGAAATAGTAAAAATGATTAGCTCTGCAGCACTTCTTTGTCCTAT
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                                        TCTGCTGAGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 859;
                                                                       Triacylglycerol lipase; corn; maize; fatty acid; seed oil;
vegetable oil; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 859 BP; 193 A; 213 C; 206 G; 245 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%; Score 529.4; DB 21;
80.6%; Pred. No. 4.8e-134;
ive 0; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                              Kinney AJ, Rafalski JA;
                                    Corn acid triacylglycerol lipase cDNA contig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the enzyme in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                Location/Qualifiers
1..858
/*tag= a
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                                                                                                                                                                                                                                                                                                                  99WO-US09280
                                                                                                                                                                                                                                                                                                                                                    980S-0083688
(first entry)
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Matches 644; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-062036/05.
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28-FEB-2000
                                                                                                                                                                                                                                                                                                                  29-APR-1999;
                                                                                                                                                                                                                                        WO9955883-A2
                                                                                                                                                                                                                                                                                                                                                    30-APR-1998;
                                                                                                                                                                                                                                                                             04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              Cahoon EB,
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This is the nucleotide sequence of a contig assembled from the entire cDNA insert in clone sre.pk0004.d7 and a portion of the cDNA insert in clones sls1c.pk009.02 and srr1c.pk001.m19 encoding the entire soybean cold triacy1g1ycerol lipses (TAGL) (see ANY32310). The clones were isolated from root and Sclerotinia sclerotiorum infected soybean cDNA libraries. Novel acid and neutral TAGL polypeptides (see ANY32301-17) and polynucleotides (see ANZ450-66) from corn, catalpa, rice, soybean and wheat tissues are disclosed. The enzymes may be prepared recombinantly and used to raise antibodies, which care used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacy1g1ycerol and choiserery1 esters found in those cells. Accumulation of fatty acids with nursual structures may be desirable to eliminate expression of TAGL genes for cartain applications. TAGL enzymes may also be useful for the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the useful as herbicides. This is desirable because inhibition of the structure of the enzymes could lead to an inhibition of the create activity of either of the enzymes could lead to an inhibition of plant process. The plynucleotides also serves as a source of probes and primers, which are useful for genetic mapping, as markers for traits in and the isolate homologous sequences from other and the could be and to isolate homologous sequences from other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 AACAAAAGATGGATTCCTTTTATCTTTCAGCATATCCCACATGGCAAAAATAAAGCAGC 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 AGACACATGGTTCATAAACTCTGCTGAGCAATCACTTGGGTATATCCTTGCTGATAACGG
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                                                                                                                                      Cahoon EB, Cahoon RE, Kinney AJ, Rafalski JA;
                                                                                                                                                                                                                                                                          of the enzyme in transgenic plants
                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                      Claim 2; Page 50; 65pp; English.
99WO-US09280
                                            980S-0083688
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Matches 708; Conservative
                                                                                                                                                                                2000-062036/05.
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29-APR-1999;
                                            30-APR-1998;
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1054 GCCCATATGGATGGGATATGGAGGTCTTGATGCATTGGCTGATGTAACCGATGTTCAGCG 1113
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                                                                                                                                                                                                                                                                                                                     514 ITTAGCAATGCTAGGCTATGTGTATACAGTCACACAGTCCAAAATTCTATATGTGGGGCA
            TAGCTCTGCAGCACTTCTTTGTCCTATTTCTTATCTTGATCATGTTAGTGCTAGTTTTGT
                                                                                                                               TCTCAGAGCAGTCGCCATGCATCTTGATCAGATGCTTGTTACTATGGGAATTCACCAGCT
                                                                                                                                          GAACTTCCGTAGCGACATGGGGGTTCAAATAGTAGATTCTTTGTGCGATGGTGAACACGT
                                                                                                                                                                                        GGATTGCAACAATTTGCTATCTGCGATTACAGGGGAAAACTGTTGCTTCAATACATCAAG
                                                                                                                                                                                                                                 TTTTCAGATGATCAGGAAAGGCACTTTCGCAAAGTATGACTATGGGTTATTGGGAAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                     1114 TACTATCAGAGAGCTGGGATCTACACCAGAACTTCTGTACATTGGTGACTATGGCCATAT
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                                          TTCACAGGGAACTATAATGGGTTTGGCGCTTTGACGATGCCCGAAATAGTAAAAATGAT
                                                                                                          TGAGGCTGCAGCTCTTCTATCTCCAATATCATACTTGGATCATGTCAGTGCACCTCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triacylglycerol lipase; soybean; fatty acid; seed oil; vegetable oil; transgenic plant; ss.
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184..1416
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                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of a contig assembled from the entire cDNA insert in clone ssl.pk0022.al and a portion of the cDNA insert in clone ssl.pk0022.al and a portion of the cDNA insert in clone sdp3c.pk004.n3 encoding the entire soybean acid triacylglycerol lipase (TAGL) (see AAY32309). The clones were isolated from soybean developing pod and seedling (5-10 day post germination) cDNA libraries. Novel acid and neutral TAGL polypeptides (see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn, catalpa. rice, soybean and wheat tissues are disclosed. The enzymes may be prepared recombinantly and used to raise antibodies, which are used for detecting the enzymes in situ in cells or in vitro in cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lower levels than normally out in cell types or developmental processes where they are not normally found. This would alter the level of triacylglycerol and cholesteryl esters found in those cells. Accumulation of fatty acids with nursual structures may be a positive phenotype in plants used for foods. In addition, it may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be used a for formal accessing of plant seed oils. The TAGL enzymes can also be used as targets to facilitate the cells in a hearthcides. This is desirable because inhibition of the arymes could nay the anymes could hard to an inhibition of the arymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1718 BP; 492 A; 353 C; 344 G; 529 T; 0 other;
                                                                                                                                                    Cahoon RE, Kinney AJ, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 184.6; DB 2 Pred. No. 8.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                             Claim 2; Page 48; 65pp; English.
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12.4%;
Best Local Similarity 51.1%;
Matches 489; Conservative
                                                           99WO-US09280
                                                                                         980S-0083688
                                                                                                                                                                                  2000-062036/05
                                                                                                                                                                                                  P-PSDB; AAY32309
W09955883-A2
                                                           29-APR-1999;
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Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCGCTACGGTCATTTGCGTCCTCCCGCATTTGACCTAAGCAGCATACCAGAATCACTG 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCATGATAAGCTTTTCTGGGATTGGAGCTGGCAAGAGTTAGCTGAATATGACCTTTTA
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                                                          610 CCCTCTAGCCAGGCCTATTGGAATTGGTCTTGGGATGAACTTGTCTCCTATGATTTCCCT
                                                                                                                                                                                          670 GCGGTGTTTAATTATGTGTTCAGCCAAACGGGGCAGAAGATCAATTACGTTGGCCATTCA
                                                                                                                                                                                                                                                           578 CAGGGAACTATAATGGGTTTGGCGGCTTTGACGATGCCCGAAATAGTAAAAATGATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 AGAGCAGTCGCCATGCATCTTGATCAGATGCTTGTTACTATGGGAATTCACCAGCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  910 CCAAAAGGGTTAGCTGTTGATGCCTTTCTCAAGTCTCTCTGTGCTCACCCTGGGATAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818 TGCAACAATTTGCTATCTGCGATTACAGGGGAAAACTGTTGCTTCAATACATCAAGGATT
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                                                                                                                               GCAATGCTAGGCTATGTGTATACAGTCACAGTCCAAAATTCTATATGTGGGGGCATTCA
                                                                                                                                                                                                                                                                                                                                                                                                  TCTGCAGCACTTCTTTGTCCTATTTCTTATCTTGATCATGTTAGTGCTAGTTTTGTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIB-) CHIBA PREFECTURE. (HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                                                                              AAI97406 standard; cDNA; 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2001; 2001WO-JP01629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-2001
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                                                                                                                                                                                          The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy an susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrKA genes.
                                       Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 CAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGGTGAGCAATCACTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTTTATCTCTTCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 CATATCCCACATGGCAAAATAAAGCAGCAGATAGTACTGGCCCTCCAGTT---TTTCTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGT 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 GATGAGATGGCAAAATATGACCTACCAGCTTNCATTAACTTCATTCTGAATAAAACTGGC
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                                                                                                                                                                                                                                                                                                                                                                                    Match
6.4%; Score 94.2; DB 22; Length 802;
Local Similarity 55.1%; Pred. No. 2.6e-15;
les 248; Conservative 0; Mismatches 194; Indels 8;
                                                                                                                                                                                                                                                                                                                                            Sequence 802 BP; 198 A; 177 C; 192 G; 217 T; 18 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene #3881 used to diagnose liver cancer.
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                                                                                                                                               Claim 1; Page 2526; 2979pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 248; Conservative
                                                                                                          for anti-cancer agents
WPI; 2001-565584/63
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN94855 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTGAGCAATCACTT 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTTTGGCGCTTTG 607
                                                                                                                                                                                                                                  Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 94.2; DB 24; Length 2481;
55.2%; Pred. No. 4.6e-15;
ive 0; Mismatches 193; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2481 BP; 692 A; 477 C; 513 G; 799 T; 0 other;
                                                                                                                                                         Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3881; 298pp; English.
                                                                                                                                                         Peres-Da-Silva
                                    02-OCT-2001; 2001WO-US30589.
                                                                          02-OCT-2000; 2000US-237054P.
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                                                                                                                   (GENE-) GENE LOGIC INC
                                                                                                                                                         Alvares C,
                                                                                                                                                                                                                                                                                               liver tissue sample
                                                                                                                                                                                              WPI; 2002-426119/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 249; Conserv
11-APR-2002
                                                                                                                                                         Horne D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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473 GATGAGATGGCAAAATATGACCTACCAGCTTCCATTAACTTCATTCTGAATAAAACTGGC
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                                                                                                                                                                                                                                                                      /*tag= a
/product= "
68..124
                                                                                                                                                                                                                                                                                                /*tag= b
125..1258
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bolen PL, Cihak PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-424751/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABB76189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               food products.
                                                                                                                                                                                                                               Capra hircus
                                                                                                                                                                                                                                                                                                                                                                                05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998;
                                                                                                                                                                    05-AUG-2002
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                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                ABL57144;
                                                                                                                                                                                                                                                   Key
                                                                                                          RESULT 8
                                                                                                                     ABL5714
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                                      g
                                                          δλ
                                                                          QQ
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                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PPCA restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTTTATCTTTCAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 CATATCCCACATGGCAAAAATAAAGCAGCAGATAGTACTGGCCCTCCAGTT---TTTCTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTGAGCAATCACTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 GGATTCCCTAGTGAGGAATACCTAGTTGAGACAGAAGATGGATATATTCTGTGCCTTAAC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 CAACATGGCTGGCTGGCAGATTCTAGTAACTGGGTCACAAACCTTGCCAACAGCAGCCTG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 CAAGAGTTAGCTGAATATGACCTTTTAG---CAATGCTAGGCTATGTGTATACAGTCACA 547
                                                                                                                                                                                                                                                                      Sakurada K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                them
                                                                                                                                                                                                                                                                                                                              sequences, proteins encoded by them and antibodies against ful in diagnosis and treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%; Score 94.2; DB 22; Length 2493; 55.2%; Pred. No. 4.6e-15; ive 0; Mismatches 193; Indels 9;
                                                                                      65.
                                                                                                                                                                                                                                                                      Kawabata A,
                                                                                                        shear stress-response protein; vascular disease;
                                                                                     Human shear stress-response coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2493 BP; 692 A; 484 C; 516 G; 801 T; 0 other;
                                                                                                                                                                                                                                                                    M, Ota T,
Sugano S;
                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 398-402; 678pp; Japanese.
                                                                                                                                                                                                                                                                     H, Obayashi
Nakamura Y,
                          AAH02906 standard; DNA; 2493 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                02-OCT-2000; 2000WO-JP06840
                                                                                                                                                                                                                   99JP-0280976.
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.2
Matches 249; Conservative
                                                                                                                                                                                                                                                                   Yoshisue
                                                                                                                                                                                                                                                                                               WPI; 2001-266308/27
P-PSDB; AAB90783.
                                                                                                                                                                                                                                                                             Sekine S,
                                                                                                       Human; shear stres
arteriosclerosis;
                                                                                                                                                                                                                                                 NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                                                                                                                  arteriosclerosis
                                                                                                                                                        WO200125427-A1
                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              hypertension.
                                                                                                                                                                                                                   01-OCT-1999;
                                                                15-JUN-2001
                                                                                                                                                                            12-APR-2001.
                                                                                                                                                                                                                                                                    Nojima H,
Kuga T, S
                                              AAH02906;
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The present sequence is a nucleic acid encoding kid goat pregastric esterase (kPGE, see ABB76189). kPGE free of other goat proteins can be produced by purification from the kid gullet or by recombinant expression in a non-kid cell, especially an Escherichia coli, expression in a non-kid cell, especially an Escherichia coli.

Caccharomyces cerevisiae (NRRL Y-30030) or CHO cell (all claimed). kPGE may be produced with an N-terminal polyHis-enterokinase sequence, which increases kPGE expression. The kPGE can be used to treat animals with an esterase or lipase deficiency. The enzyme produces a mixture of fatty acids when reacted with a dairy product, such as lipolysed butter oil, milk, cheese or whey. It is therefore useful in the production of enzyme modified cheeses as a substitute for rennet, and in the creation of flavour in cheese foods or any other food containing tridlycerides. Microbial production will allow the development of new Kosher and vegetarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An isolated kid goat pregastric esterase free from other goat proteins is useful to prepare enzyme modified cheese and to treat animals with an esterase or lipase deficiency \,\cdot\,
                                               548 CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTTTGGCGGCTTTG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Esterase; lipase; enzyme; goat; rennet; cheese; flavour; gene; ss.
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                                                                                                                                                            Disclosure, Column 27-28; 35pp; English.
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58..1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kid goat pregastric esterase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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Query Match
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ABK86570
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                                                                                                                                                                                                                                                                                                                         430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547
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                                                                                                                                                                                                                                          CAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTGAGCAATCACTT 370
                                                                                                                                                                                                                                                                 TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
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                                                                                 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAGATGGATTCCTTTTATCTTTCAG 253
                                           Gaps
                                                                                                       CGGATTCCTCATGGAAAGAATGATGTAATCATTTAGGTCAGAGACCTGTTGTGTTTCTG
                                                                                                                                                                                                                                                                                                                                              GGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCTATGTGT----ATACAGTCACA
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                                           9
Length 1411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qs
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector; YE-1; esterase; lipase; goat; cheese; flavour;
    DB 24;
                                         0; Mismatches 188;
  6.1%; Score 91.2; 54.2%; Pred. No. 2.3
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                                           230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-424751/45
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               608 ACGA 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL57145;
  Query Match
                           Best Local
                                         Matches
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ABL57145
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CGGATTCCTCATGGAAAGAATGATGCTAATCATTTAGGTCAGAGACCTGTTGTGTTTCTG 1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATATCCCACATGCCAAAATAAAGCAGCAGCAGAT---AGTACTGGCCCTCCAGTTTTTCTT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAGATGGATTCCTTTATCTTCAG 253
                        transform a host cell, such as Saccharomyces cerevisiae, for recombinant production of kPGE. The recombinant kPGE can be used to treat animals with an esterase or lipase deficiency. The enzyme produces a mixture of faty acids when reacted with a dairy product such as lipolysed butter oil, milk, cheese or whey. It is therefore useful in the production of enzyme modified cheeses as a substitute for rennet, and in the creation of flavour in cheese foods or any other food containing triglycerides. Microbial production will allow the development of new Kosher and vegetarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1898 GATGAAATGGCTGAATATGACCTTCCATCTACAATTGATTTCATCTTAAAGAGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCTATGTGT - - - ATACAGTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTTTGGCGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8324;
see ABB76189) can be used to
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8324 BP; 2394 A; 1884 C; 1703 G; 2343 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5.7e-14;
; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.1%; Score 91.2; DB 2.54.2%; Pred. No. 5.7e-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
pregastric esterase (kPGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK86570 standard; cDNA; 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 ACGA 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Simi
Matches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK86570;
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WO200236731-A2
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                                                                                                                                                                                                                                                                                                                                                                             ABK86569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder
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                                                                                                       537
                                                                                                                                             443
                                                                                                                                                                                                                                                                                           RESULT 11
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Dolypeptide. Also included are the polynucleotide encoding the
lipase (or its fragment, derivative, allete or sequence at least 60%
defection into it), vectors, host cells, a reagent (e.g. an antisense oligonucleotide) which binds to the lipase or polynucleotide (used for detection and modularing/reducing the lipase activity) and an anti-lipase antibody. The lipase and polynucleotide are useful for identifying the lipase and polynucleotide are useful for identifying the interest and interest and polynucleotide are useful for createment of a disease such as lipid malabsorption illness, cystic fibrosis, alcoholism, heart disease, heart attack, wolman disease, cholesterol eater storage disease, brain injury, mood disorder, anxiety disease thought disorder, volition disorder, sleep disorder, neurogenic disorder, myopathic disorder, obscity, cancer, corroint obscruttive pulmonary disease (COPD), diabetes, cancer, anxiety disease (COPD), diabetes, cancer, anxiety disorder, adisorder, adisorder, adisorder, adisorder, actual disorder, adisorder, anxiety disease, parkinson's disease, context adisorder, actual nervous system disorder and anorexia, osteoarthritis, a central nervous system disorder and context and any parking disorder, and propriet and any parking disorder, only appropriate and anorexia, osteoarthritis, a central nervous system disorder and context and any parking disorder. The present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 TCCTGCCACTCGGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGAAACGCCTGGTCTCGAAAACACAAGACACTCTCCATAGACCAAGATGAGTTCTGGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 TCCAACATCAAGGCTATCCCTGTGAGGAATATGAAGTCGCAACTGAAGATGGGTATATCC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 TATCTCTTCAGCATATCCCACATGGCAAAATAAAGCAGCAGATA---GTACTGGCCCTC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 TITCIGITAACAGGATICCTCGAGGCCTAGIGCAACCIAAGAAGACAGGITCCAGGCCIG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 CAGTITITCITCAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAATAGCCTGGGCTTCATTCTGGCAGATGCTGGTTTTGACGTGTGGGATGGGGAACAGCA 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human lysosomal acid lipase polypeptide, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          obesity, chronic obstructive pulmonary disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, diabetes, obesity, chronic obstructive pulmonary disease peripheral or central nervous system disorder or cardiovascular
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                                                            "Lysosomal acid lipase #2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding human lysosomal lipase #2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 4; 126pp; English.
                                                                                                                                                                                  30-OCT-2001; 2001WO-EP12518
                                                                                                                                                                                                                           31-OCT-2000; 2000US-244170P.
29-MAY-2001; 2001US-293516P.
                                      /*tag= a
/product=
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                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG
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                                                                                                  WO200236731-A2
                                                                                                                                           10-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                Xiao Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
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Key
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polypeptide. Also included are the polymucleotide encoding the lipase (or its fragment, derivative, allele or sequence at least 60% identical to it), vectors, host cells, a reagent (e.g. an antisense oligonucleotide) which binds to the lipase or polymucleotide (used for detection and modulating/reducing the lipase activity) and an anti-lipase antibody. The lipase and polymucleotide are useful for identifying therapeutic agents that either increase or decrease the lipase activity. The identified agent, the lipase and polymucleotide are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; gene; lysosomal acid lipase; lipid malabsorption illness; cystic fibrosis; alcoholism; heart disease; heart attack; wolman disease; brain hilury; mood disorder: anxiety disorder; thought disorder; volition disorder; sleep disorder; neurogenic disorder; myopathic disorder; cobesity; cancer; chronic obstructive pulmonary disease; diabetes; cardiovascular disorder; Alzheimer's disease; Parkinson's disease; peripheral nervous system disorder.
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                                                                                                                                                                                                       480 ATTGGAGCTGGCAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCT---ATGTGT
                                                                      383 CTTTCAGTTATGATGAGATGGCTAGGTTTGACCTTCCTGCAGTGATAAACTTTATTTTGC
                                                                                                                                                         ATACAGTCACACAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTT
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/product= "Lysosomal acid lipase #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding lysosomal acid lipase #1.
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1..1197
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2001US-293516P.
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                                                                                                                                                                                                                                                                                                                   611
                                                                                                                                                                                                                                                                                                                   597 TGGCGGCTTTGACGA
                                                                                                                                                                                                                                                                                                                                                                                                  503 TTATTGCATTTTCCA
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24-MAY-2000; 2000WO-US14858.
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ID AAD1
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treatment of a disease such as lipid malabsorption illness, cystic fibrosis, alcoholism, heart disease, heart attack, Molman disease, cholesterol ester storage disease, brain injury, mood disorder, anxiety disorder, thought disorder, volition disorder, sleep disorder, neurogenic disorder, myopathic disorder, obesity, cancer, chronic obstructive pulmonary disease (COPD), diabetes, cardiovascular disorder, Alzheimer's disease, Parkinson's disease, anorexia, osteoarthritis, a central nervous system disorder and a peripheral nervous system disorder. The present sequence is the CDNA encoding human lysosomal lipase #1.
                                                                                                                                                                                                                     242
                                                                                                                                                                                                                                                                                                                                                                                                                        479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596
                                                                                                                                                                                                                                              TCCAACATCAAGGCTATCCCTGTGAGGAATATGAAGTCGCAACTGAAGATGGGTATATCC 142
                                                                                                                                                                                                                                                                      243 TATCTCTTCAGCATATCCCACATGGCAAAATAAAGCAGCAGATA---GTACTGGCCCTC 299
                                                                                                                                                                                                                                                                                                                     300 CAGTITITCTTCAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTG 359
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                    TCCTGCCACTCGGCTACCCCTGCACCGAGCACGTTGAAACAAAAGATGGATTCCTTT
                                                                                                                                                                                                                                                                                                                                     TITCTGTTAACAGGATTCCTCGAGGCCTAGTGCAACCTAAGAAGACAGGTTCCAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                               263 ACAATAGCCTGGGCTTCATTCTGGCAGATGCTGGTTTTTGACGTGTGTGGGGATGGGAACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGAAACGCCTGGTCTCGAAAACACACACTCTCCATAGACCAAGATGAGTTCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGAACGCGTTGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTTCTGGG
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                                                                                                                                                                   DB 24; Length 1210;
                                                                                                                                                                Score 89.4; DB 24; Length
Pred. No. 6.5e-14;
0; Mismatches 196; Indels
                                                                                                                                         Sequence 1210 BP; 338 A; 264 C; 296 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                   6.0%;
                                                                                                                                                                               53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                           Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATTGCATTTTCCA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCGGCTTTGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 ORF.
                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-2000,
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                                                                                                                                                                    Query Match
                                                                                                                                                                                 Best Local
                                                                                                                                                                                                                                             83
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The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see ARF45121-F45136 and AAR45138-F45139 and AAB660857, AAB660864-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders, but as system (CNS) disorders, CNS-related disorders, focal nearly system (CNS) disorders, CNS-related disorders, focal neurological and cerebrovacular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, anxiety, and bipolar affective disorder.
                                                                                                                                                                                                                                                                                                                                                    TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCC 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGCCACTCGGCTACCCCTGCACCGAGCACATGAAACAAAAGATGGATTCCTTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCAACATCAAGGCTATCCCTGTGAGGAATATGAAGTCGCAACTGAAGATGGGTATATCC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCTGTTAACAGGATTCCTCGAGGCCTAGTGCAACCTAAGAAGACAGGTTCCAGGCCTG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGTTACTGCAGCATGGCCTAGTTGGAGGTGCTAGCAACTGGATTTCCAACCTGCCCA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCTCTTCAGCATATCCCACATGGCAAAAATAAAGCAGCAGATA---GTACTGGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 CAGITITICITCAACAIGGICITITITCAGGGAGGAGACACAIGGITCAIAAACICIGCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGAACGCGTTGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTTCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1269 BP; 358 A; 268 C; 309 G; 334 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 89.4; DB 22;
Pred. No. 6.6e-14;
0; Mismatches 196;
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                                                                                                                                                              Barnes
                                                                                                                                                      Sharp JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 6; 359pp; English.
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                                                                         (MILL-) MILLENNIUM PHARM INC
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Best Local Similarity 53.6
Matches 233; Conservative
                                                                                                                                                          McCarthy SA, Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATTGCATTTTCCA
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14-JUN-1999;
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304 TCCAACATCAAGGCTATCCCTGTGAGGAATATGAAGTCGCAACTGAAGATGGGTATATCC 363

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, coronary artery thrombosis and cerebral artery thrombosis or intracardiac thrombosis and stroke. The nucleotides of the invention are used in gene therapy. The present sequence is human CG162 (or C59)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein receptor polypeptides, useful for preventing diagnosing and treating lipiq metabolism disorders, thrombosis and cardiovascular diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodrich R;
                                                                                                                                                                             Human, apolipoprotein; lipase; lipoprotein receptor; ALLr; angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1384 BP; 404 A; 281 C; 328 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang TY,
Drmanac 1
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Zhao QA, Wehrman T,
                                                                                                                                                                                                                                                                                                                                           neuroprotectant; cerebroprotective; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 160-161; 266pp; English.
                                                                                                                       (or C59) lipase DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0598042.
2000US-0631451.
2000US-0667298.
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                                                         (first entry)
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Asundi V, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611724/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179446-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
22-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000;
                                                         18-DEC-2001
                                                                                                                       Human CG162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2001
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AAD19220;
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/product= "Human mature CG162 (or C59) lipase protein"
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                                                                                                                                                                                                                                                                                                                               596
                                                                                                                                                                                                                                                                                                                                                 CAGTTTTTCTTCAACATGGTCTTTTTCAGGGAGGACACATGGTTCATAAACTCTGCTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
cardiovascular disease; lipid metabolism; myocardial infarction;
cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coronary artery thrombosis; cerebral artery thrombosis; strokė; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator; neuroprotectant; cerebroprotective; ds.
TATCTCTTCAGCATATCCCACATGGCAAAATAAAGCAGCAGATA---GTACTGGCCCTC
                                                                                                                                                              ACAATAGCCTGGGCTTCATTCTGGCAGATGCTGGTTTTGACGTGTGGGGTATGGGGGAACAGCA
                             364 TITCTGITAACAGGATICCICGAGGCCTAGIGCAACCTAAGAAGACAGGITCCAGGCCIG
                                                                                            424 TGGTGTTACTGCAGCATGGCCTAGTTGGAGGTGCTAGCAACTGGATTTCCAACCTGCCCA
                                                                                                                                                                                                                             544 GGGGAAACGCCTGGTCTCGAAAACACAAGACACTCTCCATAGACCAAGATGAGTTCTGGG
                                                                                                                                                                                                                                                              480 ATTGGAGCTGGCAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCT---ATGTGT
                                                                                                                                                                                                                                                                                             604 CTTTCAGTTATGATGAGATGGCTAGGTTTGACCTTCCTGCAGTGATAAACTTTATTTTGC
                                                                                                                                                                                                                                                                                                                               ATACAGTCACACAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTT
                                                                                                                               AGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCC
                                                                                                                                                                                             GTGGAACGCGTTGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human CG162 (or C59) lipase protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotectant; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human CG162 (or C59) lipase DNA #2.
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2000US-0598042.
2000US-0631451.
2000US-0667298.
2000US-0714936.
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189..245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              597 TGGCGGCTTTGACGA 611
                                                                                                                                                                                                                                                                                                                                                                                                                              724 TTATTGCATTTTCCA 738
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03-AUG-2000;
22-SEP-2000;
17-NOV-2000;
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243
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AAD19226
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Indels

Length 1384;

6.0%; Score 89.4; DB 22; 53.6%; Pred. No. 6.9e-14; 0; Mismatches 196; 183 TCCTGCCACTCGGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTT 242

Conservative

Best Local Similarity

Query Match

233;

Matches

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(HYSE-) HYSEQ INC

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The invention relates to polynucleotides encoding proteins CG122, CG179, CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human apolitoporoteins. Ilpases and lipoprotein receptor proteins. These DNA and protein sequences are useful for treating or preventing disorders associated with apolitoporoteins, lipases and lipoprotein receptor (ALLr) expression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for expression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for identifying a cuseful for identifying a disease associated with altered levels of these sequences. ALLr polypeptides are also useful for useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALLr proteins. The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular thrombosis. Coronary artery thrombosis and cerebral artery thrombosis of the invention are used in gene therapy. The present sequence is human CG162 (or C59)
                                                                                                                                                                                                     Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein receptor polypeptides, useful for preventing diagnosing and treating lipid metabolism disorders, thrombosis and cardiovascular diseases -
                                                                     Qian XB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                               Goodrich
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                                             fang TY, Zhou P, Go
Drmanac RT, Ren F,
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                                               Tang TY,
                                          Montgomery JR,
QA, Wehrman T,
                                                                                                                                                                                                                                                                                                  Claim 1; Page 183-185; 266pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%;
Best Local Similarity 53.6%;
Matches 233; Conservative (
                                                                  Zhao QA,
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Asundi V, Zl
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P-PSDB; AAE11931.
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                                                                            304 TCCAACATCAAGGCTATCCCTGTGAGGAATATGAAGTCGCAACTGAAGATGGGTATATCC 363
                                                                                                                    TATCTCTTCAGCATATCCCACATGGCAAAATAAAGCAGCAGATA---GTACTGGCCCTC 299
                                                                                                                                                        364 TITCIGITAACAGGATICCICGAGGCCIAGIGCAACCIAAGAAGACAGGITCCAGGCCIG 423
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Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease; senile dementia; Huntington's disease; sanyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAR45138-F45139 and AAB66031-B66057, AAB66004-B660033 and AAB660085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 TCCTGCCACTCGGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 8.5e-14;
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                                                                                                                                                                                                                AAF45131 standard; cDNA; 2044
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Local Similarity 53.6%;
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BIO369642 SAE55604
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE443524 117 bp mRNA linear EST 25-JUL-2000 WHE1115_C05_F09ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1115_C05_F09, mRNA
BQ122157 EST607733
BM501471 PAC000000
AU161807 AU161807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, P
West Area, Western Regional Research Center
West Area, Western Regional Research Center
West Area, Western Regional Research Center
Tel: 5105555773
Fax: 5105595818
Email: condersnépw.usda.gov
Sequence have been trimmed to remove vector sequence and low
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Anderson, O.D., Chao, S.
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BI075779 IPI_21_B0
BE367129 PII_43_D1
AU088737 AU088737
BM037885 S113f11 S
                                                                                                                 (without alignments)
10789.716 Million cell updates/sec
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                                                                                                                                                                                        Description
                                                                                                  Search time 2226 Seconds
                                                                                                                                                                                                                                                                                          32308132
            version 5.1.3
- 2002 Compugen Ltd
                                                                                                                                                                                                                                                              16154066 segs, 8097743376 residues
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Maximum Match 100%
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Copyright (c) 1993
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                                                                     nucleic search, using
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                                                                                                                                                                                                                                                                                                                                                                     FICI_24_G11.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum bicolor cDNA, mRNA sequence.
BM324154
BM324154
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EST.
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sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences have been trimmed to exclude PolyA, vector, and regions below phread quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. T7 sequencing primer, are presented as the reverse complement. High quality sequence stop: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R., Sudman,M. and Pratt,L.H.
An EST database from Sorghum: plants infected with a compatible
547 GAGCGATATGGGAGTTCAAATAGTAGATTCTATATGCGATGATGGACATGTGGACCTGCAA. 606
                                                                                                                           Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sorghum bicolor"
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/db_xref="taxon:4558"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
                                                                                            DB 13; Length 623;
                                                                                                                                                                                                                                          666 TTACTTGGAGTACGAACCTCATCCATCTTCAACTAAAAACTTGCATCATT 717
                                                                                                                                                                                                                 TTATTTGGAGTATGAACCTCATCCATCATCGACAAAAAATCTGCACCATCTT 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
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                                                                                                                                                                                                                                                                                                                                                                              // Anotes Weetor: Landard Uni-ZAP XR, excised phagemid phages. Cont. Cont. Cont. Site. 1. ECORI; Site. 2: XNOI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The CDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                  /cultivar-"Chinese Spring"
/db_xref="taxon:4555"
/clone="WHE1115_C05_F09"
/clone="WHeat etiolated seedling root normalized cDNA library"
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/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
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   quality sequence with phred score less than 20
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86.7%; Pred. No. 9.3e-118;
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                                 Stratagene SK primer.
                                                          Location/Qualifiers
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/db_xref="taxon:4558"
/clone_lib="Immature pannicle 1 (IPl)"
/clone_lorgan: Developing preanthesis pannicles; Vector:
pBluescript II $$K(-)$ from Lambda Zap II; $$tte_1: XhOI;
$$ite_2: EcorI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

175 c 175 g 171 t 1 others
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Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with PolyTMix or T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 572 POLYA-NO.
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                                                                                                                                                                                                                                                                                             Score 403; DB 13;
Pred. No. 1.5e-83;
); Mismatches 126;
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                                                                                                                            /organism="Sorghum bicolor"/cultivar="BTx623"
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78.98;
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Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidese; Andropogoneae; Sorghum.
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BIO75779
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                                                                                                                                                                                 180
                                                                                                 AGGGAGGAGACACATGGTTCATAAACTCTGCTGAGCAATCACTTGGGTATATCCTTGCTG 386
                                                                                                                 446
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                                                          ATAACGGTTTTGATGTTTGGGAATGTCCGTGGAACGCGTTGGAGTAAAGGTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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                    Indels
    6.4e-98;
thes 99;
                 0; Mismatches
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9
     Pred.
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    84.1%;
                  524; Conservative
    Local Similarity
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DEFINITION
                  Matches
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KEYWORDS
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Organ sativa (japonica cultivar-group).

Organ sativa (japonica cultivar-group).

Organ sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Organea; Organ.

1 (bases 1 to 478)

Sasaki,T. and Yamamoto,K.

Rice cDNA from eticlated shoot (2000)

Onpublished (2000)

Ontact: Tawiji sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 bp mRNA linear EST 02-APR-2 Rice shoot Oryza sativa (japonica cultivar-group) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305-8602, Japan
Tel: 81-298-38-7441
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                      GGGATATGGAGGTCTTGATGCATTGGCTGATGTAACCGATGTTCAGCGTACTATCAGAGA 1125
    946 CAGGAAAGGCACTTTCGCAAAGTATGACTATGGGTTATTGGGAAACCTAAGGCGCTACGG 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                          1006 TCATTTGCGTCCTCCCGCATTTGACCTAAGCAGCATACCAGAATCACTGCCCATATGGAT
                                                                                                          DB 9; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Rice shoot"
/dev_stage="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
148 c 120 g 110 t 2 others
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Pred. No. 6.8e-73;
0; Mismatches 18;
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llarity 94.6%;
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/clone_lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 62)
cultivar) were infected with pathogen (isolate FRW42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly. A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                     sorghum.
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                to exclude PolyA, vector and regions threshold for highest quality sequence
PI1_43_D12.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGGAGTATGAACCTCATCCATCACGACAAAAATCTGCACCATCTTTTCACATGAT 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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An EST database from Sorghum: pathogen-induced plants
Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 360; DB 10; Length 491; 83.6%; Pred. No. 1.7e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Sorghum bicolor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: JEN REV
High quality sequence stop: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed
below Phred quality 16. The
                       mRNA sequence.
BE367129
BE367129.1 GI:9308686
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the pathogen.
104 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 408; Conservative
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EST 02-APR-2002

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939 A-GATGATCAGGAAAGGCACTTTCGCAA----AGTATGACTATGGGTTATTGGGAAACC
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/db_xref="taxon:3880"
/clone="pGLSD-28123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Medicago truncatula
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                             EST 06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryzae.

1 (bases 1 to 631)

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, F.F., Jang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

Gene Expression Screen in Oryza sativa
Unpublished (2001)
           248
                                 262
                                                         307
                                                                                322
                                                                                                          367
                                                                                                                                 382
                                                                                                                                                         426
                                                                                                                                                                     820 CAACAATTTGCTATCTGCGATTACAGGGGAAAACTGTTGCTTCAATACATCAAGGATTGA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                            BM037885
S113f11 Stem library from Oryza sativa (3-5 leaf stage) Oryza
sativa cDNA clone S113f11, mRNA sequence.
                                                       CTTCAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATAAACTCTGCTGAGCAATCA
                                                                                                                   CTTGGGTAT - ATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 341.6; DB 13; Length 631;
Pred. No. 3.3e-69;
0; Mismatches 65; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Dong HT
Laboratory of Functional Genetics
Blo-technology Institute of Zhejiang University
Raixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Eax: 0086-571-86961525
Email: htdongézjuem.zju.edu.cn
Seg primer: M13 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/note="Vector: pSport2"
117 c 153 g 174 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="S113f11"
                                                                                                                                                                                                                                                                                                                              BM037885
BM037885.1 GI:16753506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.0%;
Best Local Similarity 84.7%;
Matches 466; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa.
Oryza sativa
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JOURNAL '
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                               203
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BM037885
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828 bp mRNA linear EST 17-APR-2002
EST607733 GLSD Medicago truncatula cDNA clone pGLSD-28123, mRNA
Sequence.
B0122157
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
                                          1048
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TIGR sequence name: MTRAA60TK More information is available at:
www.medicago.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                         365
                                                                                                                                                                                                                                                             425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTS from late stage developing seeds of Medicago truncatula Unpublished (2002)
Contact: Grusak, M.A.
CORDAARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Fax: 713 798 7044
                                                                                                                                                                                                                                                                                                                                                                                           186 AGGAGGATTCAGAAAGGCACTTTCGCCAAAGTNATGACTATTGGGGTTATTGGGGAAACC
                                          TAAGGCGCTACGGTCATTTGCG-TCCTCCCGCATTTGACC---TAAGCAGCATACCAGAA
                                                                                                                            1049 TCACTGCCCATATGGATGGGATATGGAGGTCTTGATGCATTGGCTGATGTAACCGATGTT
                                                                                                                                                                                                                    CAGCGTACTATCAGAGAGCTGGGATCTAC - ACCAGAACTTCTGTACATTGGTGACTATGG
                                                                                                                                                                                                                                        /tissue_type="Immature seeds"
/dev_stage="25 to 35 days after pollination"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ςς)·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: SKmod (CTA gAA CTA gtg gAT
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XhoI; Immature seeds, collected from pods ranging in age from 25 to 35 days after pollination, were harvested from greenhouse-grown plants. Seed were removed and separated from pod walls and immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOIR cells."
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                                                                                                                                                                                                                                                                                                                          350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCTTGATCAGATGCTTGTTACTATGGGAATTCACCAGCTGAACTTCCGTAGCGACATG 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGTTCAAATAGTAGATTCTTTGTGCGATGGTGAACACGTGGATTGCAACAATTTGCTA 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 GGCCCTCCAGTTTTTCTTCAACATGGTCTTTTTCAGGGGAGGAGACACATGGTTCATAAAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               708 CAAGAACCTCACCCATCATCCTCCAAAAACTTGAACCATTTTCCAGATGATCCGCAAA 767
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                      TCTGCTGAGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGG
                                                                                                                                                                                                                                                                                                                                                                                         TTCTGGGATTGGAGCTGGCAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTCCGTGGAACGCGTTGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 TITTGGGATTGGAGCTGGCAAGAATTAGCCCTGTATGATCTTGCGGAAATGATCAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTATACAGTCACACAGTCCAAAATTCTATATGTGGGGGCATTCACAGGGAACTATAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTTGGCGGCTTTGACGATGCCCGAAATAGTAAAAATGATTAGCTCTGCAGCACTTCTT
                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                         DB 14; Length 828;
                                                                                                                                                                                                                                     Score 327.6; DB 14; Length
Pred. No. 6.2e-66;
0; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCACTTTCGCAAAGTATGACTATGG 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCACCTTCTCCCAGTACGATTATGG 793
                                                                                                                                                                                                                                         22.1%;
                                                                                                                                                                                                                                                      al Similarity 68.4%;
469; Conservative
                                                                                                                                                                                         228
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                        Best_Local
Matches 46
                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                      353 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
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A41 bp mRNA linear EST 14-FEB-2002 PAC000000000563 Pioneer AF-1 array Zea mays CDNA, mRNA sequence. BM501471.1 GI:18661576

> DEFINITION ACCESSION VERSION

RESULT 8 BM501471

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                                                                                           Beatty, M., Singletary, G., Hamaker, B., Larkins, B.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 bp mRNA linear EST 03-APR-. Clone S5674, mRNA sequence.
                                                                                                                                                                      Trait and Technology Development, Food and Feed Research Pioneer Hi-Bred International, Inc. 7300 NW 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA Tel: 515 270 5934 Fax: 515 254 2619 Email: rudolf.jung@pioneer.com.
                                                                                                                                                                                                                                                                                                                                                                                                                          290 ACTGGCCCTCCAGTTTTTCTTCAACATGGTCTTTTTCAGGGAGGAGACACATGGTTCATA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTCTGCTGAGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGATT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                       NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGAATGTCCGTGGAACGCGTTGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTGTCCTATTTCTTATCTTGATCATGTTAGTGCTAGTTTTTGTTCTCAGAGCAGTCGCC
                                                    Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGGTTTGGCGGCTTTGACGATGCCCGAAATAGTAAAAATGATTAGCTCTGCAGCACTT
                                                                                                                       Maize opaque endosperm mutations create extensive changes
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                                                                                                                                                                                                                                                                                                                   II; Site_2:
    others
                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 441;
                                         Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                       Streptophyta; Embryophy
yta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
/clone_lib="Pioneer AF-1 array"
/note="Vector: pSportl; Site_1: Sall;
90 c 102 g 144 t loth
                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                      Score 327.4; DB 1
Pred. No. 6.8e-66;
0; Mismatches 62
                                                    Spermātophyta; Magnoliophyta; Liliopsid
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                               /organism="Zea mays"
                                                                                                                                  patterns of gene expression
Unpublished (2002)
                                       Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                .;
0
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EST.
                                                                                                                                                                                                                                                                                                                                                                      22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCATCTTGATCAGATG 727
                                                                           1 (bases 1 to 441)
Hunter, B.G., Beatty
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                            Contact: Jung R
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                           Zea mays
                                                                                                                                                                                                                                                                                                                                  104
                                                                                                         Jung, R.
                                                                                                                                                                                                                                                                                                                                                                                                Matches 375;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350
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                                                                               REFERENCE
                                                                                         AUTHORS
                                                                                                                                                JOURNAL
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AU161807
LOCUS
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KEYWORDS
KEYWORDS
SOURCE
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/Gultuare"Extracon:455%
/Glone_lib="Pathogen-infected compatible I (PICI)"
/fissue_type="Leaves"
/dev_stage="weak-old seedlings infected with
Colletorichum grammincola"
/note="weator: pBluescript II SK(-) from Lambda Zap II;
Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRM42I, a sorghum isolate of the anthracnose
pathogen Colletorichum grammincola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the coloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."
                                                                                                                                                                                                                             Email: mmprattedga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phrea quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with PolyTMx or
T7 sequencing primer, are presented as the reverse complement.
T8 Seg primer: JBN REV
High quality sequence stop: 570
POLYA-NO.
                              EST database from Sorghum: plants infected with a compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GTCGTCTTGCTGCGGTCGCATCGTCTCCGGAGCCTCCCCAGCCGCCGCCGCCGCCTCCGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 ATCCCACATGGCAAAAATAAAGCAGCAGATAGTACTGGCCCTCCAGTTTTTCTTCAACAT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTCCTCTCCTTCCTCGCCGGTGGAGCCCGCCATCCCCGGCCACAGACGCGCTGCGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 CGCGTCGGCTCC ----- GGCTCCGGCGGCCTCTGCGACCAGCTGCTCCTGCCACTCGGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCCCTGCACCACGACGATGAAACAAAAGATGGATTCCTTTTATCTTCAGCAT 256
                                                                                                                  Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 GCGTTGGCGATGGCGATGGCGGGCCACGCCCCGGAGGGGGGCGTCCCCCTGATCCTCCTC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 324.2; DB 1
Pred. No. 3.8e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sorghum bicolor"/cultivar="BTx623"
                                                                                             Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
           Sudman, M. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.98;
                                                                            Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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ORIGIN
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                                                                          JOURNAL
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                                TITLE
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Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnollophyta: Liliopsida: Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

E 1 (bases 1 to 365)

Sasaki, T and Yamamoto, K.

Rice CDNA from etiolated shoot (2000)

L Onpublished (2000)

L Ontact: Takuji Sasaki
National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 04-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 bp mRNA linear EST 04-JAN-200 PICL_66_B12.bl_A002 Pathogen-infected compatible 1 (PIC1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 572)
Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 CCTGATCCTCCTCGTCTCTTGCTGCGGTCGCATCGTCTCCGGAGCCTCCCCAGCCGC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 ACTCGCTACCCCTGCACCGAGCACAAACGTTGAAACAAAGATGGATTCCTTTTATCTCT 249
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Calade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 CACAGCGCGGCGGCGTTGGCGATGGCGGGCCACGCCCCCGGAGGAGCGCTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xrer= run.
/clone="S6674"
/clone_lib="Rice shoot"
/dev_stage="Etiolated shoot (8 days old)"
/note="Ftiolated shoot (8 days old)"
/note="Ftiolated shoot (8 days old)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 TCAACATGGTCTTTTCAGGGAGGACACATGGTTCATAAACT 353
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98.0%; Pred. No. 3.8e-65;
Live 0; Mismatches 6;
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//dione_inb="pathogon induced 1 (PII)"
//dione_inb="pathogon induced induced leaves from
//dione_corpan: Anthracnose-infected leaves from
two-week-old sorghum plants 48 ha feter inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogon (isolate FRM42I of
Collectrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings 2 weeks old exhibit juvenile resistant
raction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass exclaion. WARNING: While
most or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                    вЕЗО/231
PI1.43.D12.92_A002 Pathogen induced 1 (PI1) Sorghum bicolor CDNA,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
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ATCCTTGCTGATAACGGTTTTGATGTTTGGATTGGGAATGTCCGTGGAACGCGTTGGAGT 436
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
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                      AAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGGATTGGAGCTGGCAAGAG
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Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum: pathogen-induced plants
                                                                                                                                                                      497 TTAGCTGAATATGACCTTTTAGCAATGCTAGGCTATGTGTATACAGT 543
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High quality sequence start: 13
High quality sequence stop: 473
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Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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FILE 24_C11.gl_A002 Pathogen-infected compatible 1 (PIC1) Sorghum BM328649
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Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with PolyTMix or
T7 sequencing primer, are presented as the reverse complement.
Seq primer: T7
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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Cordoniar-Pratty. M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,
Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1186 GAGCGTGAAGGCGAAAGATGTTTATGTGGACCTAATAAGATTTCTTAGGG---AAAA 1242
                                                                                                                                                                                                                     946 CAGGAAAGGCACTTTCGCAAAGTATGACTATGGGTTATTGGGAAACCTAAGGCGCTACGG 1005
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                                                                                                                                         241 GGGGTATGGAGGCCTTGATGCACTGGCTGACGTAACAGATGTTGAGCGCACCATCAAAGA 300
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The University of Georgia, Department of Plant Biology
That Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210

    .647
    /organism="Sorghum bicolor"
    /cultivar="BTx623"
    /db_xref="taxon:4558"

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High quality sequence stop: (
POLYA=Yes.
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Sorghum bicolor
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                                        Colletotitichum gramminicola"

Colletotitichum gramminicola"

Site_1: Xhoi; Site_2: EcoRi; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRM42I, a sorghum isolate of the anthracnose
pathogen Colletotitichum gramminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTS are expected to derive
from the host plant, no effort was made to eliminate ESTS
deriving from the pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU161802 AU161802 323 bp mRNA linear EST 03-APR-2002 AU161802 Rice shoot Oryza sativa (japonica cultivar-group) cDNA clone S5639, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1233 TTAGGG---AAAATGGATGGCATAATAGCTATTAGGATGTCTTCATGTGTATAATAAAA 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         993 TAAGGCGCTACGGTCATTGCGTCCTCCCGCATTTGACCTAAGCAGCATACCAGAATCAC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 TAAGGCACTACGGCCAGCGGCATCCTCCCTCCTTCGATCTAAGCAGCAGCATACCGGAATCAC 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      933 TTTTTCAGATGATCAGGAAAGGCACTTTCGCAAAGTATGACTATGGGTTATTGGGAAACC 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGATTGACTATTATTTGGAGTATGAACCCCATCCGTCATCAACAAAAATTTGCGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1173 TTGATTTTGTTATGAGCGTGAAGGCGAAAGATGATGTTATGTGGACCTAATAAGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1053 TGCCCATATGGATGGGATATGGAGGTCTTGATGCATTGGCTGATGTAACCGATGTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                        3;
            /tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
                                                                                                                                                                                                                                                                                                                                                                      Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTTATACTATGATGACAGTACGACTATGTAAATACGTACATA 465
                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                                     Score 294.4; DB 13;
Pred. No. 3.5e-58;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU161802.1 GI:10931528
                                                                                                                                                                                                                                                                                                                                                                   19.9%;
llarity 78.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      365;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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SOURCE
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Sasaki,T. and Yamamoto,K.
Rice cDNA from etiolated shoot (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-3441
Fax: 81-298-38-7441
Fax: 81-298-38-468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                   Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 TCAGCATATCCCACATGGCAAAAATAAAGCAGCAGATAGTACTGGCCCTCCAGTTTTTCT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An EST database from Sorghum: developing preanthesis pannicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 CCTGATCCTCCTCGTCTCTTGCTGCGGTCGCATCGTCTCCGGAGCCTCCCCAGCCGC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACAGCGCGGCGGCGTTGGCGATGGCGATGGCGGGCCACGCCCCGGAGGAGCGCTCCC 69
                                                                                                                                                                                                                                                                                                                                     (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 CGCCGCCCTCCGCCGCGCGTCGGCTCCGGCGCGCGCCTCTGCGACCAGCTGCTCCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 ACTCGGCTACCCCTGCACCGAGCACGTTGAAACAAAGATGGATTCCTTTTATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Blology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 323;
                                                                                                                                                                                                                                                                                                                                                                                               /do_xit.- 'c.....'
/clone="S5539"
/clone_lib="Rice shoot"
/dev_stage="Eticlated shoot (8 days old)"
/note="Eticlated shoot (8 days old)"
/note="Eticlated shoot (8 days old)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 646)
Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 285.8; DB 9;
Pred. No. 3.5e-56;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:14514142
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99.0%;
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                    TITLE
JOURNAL
COMMENT
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                                                  REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                    /organism="Sorghum bicolor"
/cultivar="BTx623"
/cultivar="BTx623"
/clone_lib=Tuxon.4558
/clone_lib=Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthesis pannicles; Vector:
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: ECORI; The library was made from poly-A RNA in the
cloning vector lambda ZaP II. Clones to be sequenced were
prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU088738 S.21 bp mRNA linear EST 02-APR-2002 AU088738 Rice shoot Oryza Sativa (japonica cultivar-group) cDNA clone S5305, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                    Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTMix or T7
sequencing primer, are presented as the reverse complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              999 GCTACGGTCATTTGCGTCCTCCCGCATTTGACCTAAGCAGCATACCAGAATCACTGCCCA 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1059 TATGGATGGGATATGGAGGTCTTGATGCATTGGCTGATGTAACCGATGTTCAGCGTACTA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1119 TCAGAGAGCTGGGATCTACACCAGAACTTCTGTACATTGGTGACTATGGCCATATTGATT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1179 TTGTTATGAGCGTGAAGGCGGAAAGATGTTTATGTGGACCTAATAAGATTTCTTAGGG 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 TCATCATGAGCGTGAAGGCGAAGGACGATGTTATGTTGATGATGATGATGTTTTTCATGAGGTTTTTTCAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACTACGGCCAGCGGCATCCTCCCTCATCGATCTAAGCAGCAGCATACCGGAATCACTGCCAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TCAAAGAGTTGAGATCCAGGCCAGAGCTGCTGTACATTGGTGACTATGGCCACATTGATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879 ATTATTATTTGGAGTATGAACCTCATCCATCATGACAAAAAATCTGCACCATCTTTTTC 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACTATTATTTGGAGTATGAACCCCATCCGTCATCAACAAAAATTTGCGGCATCTTTTCC 60
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      939 AGATGATCAGGAAAGGCACTTTCGCAAAGTATGACTATGGGTTATTGGGAAACCTAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 285.2; DB 13; Length 646;
Pred. No. 4.9e-56;
0; Mismatches 98; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1296 TACAGTATTGGTCCTCTCCCGATGTGGTATGTATATA 1333
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Oryza sativa (japonica cultivar-group)
                                                                                                                                               Seq primer: T7
High quality sequence start: 12
High quality sequence stop: 646
                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.2%;
Best Local Similarity 77.9%;
Matches 357; Conservative
                  Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                     POLYA-Yes.
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AU088738
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KEYWORDS
SOURCE
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta: Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae: Oryzae; Oryzae.

1 (bases 1 to 521)
Sasaki, T. and Yamamoto, K.
Rice cDNA from etiolated shoot (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                         305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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/dev_stage="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
/note="Etiolated"
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Sequence 1, Application US/09186489 Patent No. 6375947
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NAME/KEY: CDS
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## ALIGNMENTS

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APPLICANT: Bolen, Paul L.
APPLICANT: Bolen, Paul L.
APPLICANT: Scharpf Jr. Lewis G.
TITLE OF INVENTION: Processes for its Production and Use
FILE REPERENCE: 5499/3
CURRENT APPLICATION NUMBER: US/09/186,489
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1134 9 Length 1134; Indels Score 91.2; DB 4; Pred. No. 1.9e-14; 0; Mismatches 188; 6.18; Query Match 6.1 Best Local Similarity 54.2 Matches 230; Conservative

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367 GATGAAATGGCTGAATATGACCTTCCATCTACAATTGATTTCATCTTAAAGAGAACAGGA 426
                              548 CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATAATGGGTTTGGCGCTTTG 607
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bolen, Paul L
APPLICANT: Bolen, Paul L
APPLICANT: Scharpf Jr., Lewis G.
TITLE OF INVENTION: Processes for its Production and Use
FILE REPERENCE: 5499/3
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                11 CAGCATGETETTCTTGCCTCAGCTACAAACTGGATTTCCAACCTTCCGAACAACAGCCTG
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54.2%; Pred. No. 2e-14;
tive 0; Mismatches 188; Indels
                                                                                                                                                                                                 Sequence 3, Application US/09186489 Patent No. 6375947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09186489 Patent No. 6375947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Kid (Goat)
US-09-186-489-3
                                                                                            608 ACGA 611
                                                                                                                         487 TCTA 490
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US-09-186-489-3
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US-09-186-489-5
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
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Sequence 4, Application US/09186489

Sequence 4 Application US/09186489

Sequence 4, Application US/09186489

GENERAL INFORMATION:

APPLICANT: Claha, Faul L.

APPLICANT: Claha, Faul L.

TILE OF INVENTION: Purified Recombinant Kid Pregastric Esterase, and

TILE OF INVENTION: Purified Recombinant Kid Pregastric Esterase, and

TILE REFERENCE: 5499/3

TILE REFERENCE: 5499/3

CURRENT APPLICATION NUMBER: US/09/186,489

CURRENT FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 4

LENGTH: 1134

TYPE: DNA

ORGANISM: BOVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1658 CGGATTCCTCATGGAAAGAATGATGCTAATCATTTAGGTCAGAGACCTGTTGTGTTTTCTG 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1598 GGCTACCCAAGTGAGATGCATAAAGTTATAACTGCAGATGGCTATATCCTTCAGGTCTAT 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 CATATCCCACATGGCAAAAATAAAGCAGCAGAT---AGTACTGGCCCTCCAGTTTTTCTT 310
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                                                                                          Esterase,
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8324;
APPLICANT: Chark, Paul L
APPLICANT: Chark, Paul L
APPLICANT: Chark, Paul L
APPLICANT: Chark, Paul L
TITLE OF INVENTION: Purified Recombinant Kid Pregastric Ester ITILE OF INVENTION: Processes for its Production and Use FILE REFERENCE: 5499/3
CURRENT APPLICATION NUMBER: US/09/186,489
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 8324
                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 91.2; DB 4;
ilarity 54.2%; Pred. No. 4.4e-14;
Conservative 0; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Yeast YE-1 expression vector US-09-186-489-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 230;
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TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
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    350 CAGCATGCCCTGTTTGCAGACAATGCCTACTGGCTTGAGAATTATGCCAATGGAAGCCTT 409
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Patent No. 5807726
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64.4; DB 1;
Pred. No. 1.9e-07;
0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620-033
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869-8084/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.3%;
Best Local Similarity 49.8%;
Matches 220; Conservative C
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MOLECULE TYPE: cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
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STRANDEDNESS: double
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ADDRESSEE: Pennie &
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1RY: U.S.A.
10036
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US-08-227-108-2
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US-08-227-108-2
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APPLICANT: MERKULOV, Gennady et al
APPLICANT: MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE OF INVENTION: THEREN OF FILE REFERENCE: CL001186
FILE REFERENCE: CL001186
CURRENT APPLICATION NUMBER: US/09/820,001
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                        187 CAGCATGGTCTTCTTGGATCAGCCACAACTGGATTTCCAACCTGCCCAAGAACAGCCTG 246
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                                                                                                                             194 GGCTACCCCTGCACCGAGCACAACGTTGAAACAAAAGATGGATTCCTTTATCTTTCAG 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTTTTCTGGGATTGGAGCTGG 490
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                                        5.9%; Score 88; DB 4; Length 1134;
53.8%; Pred. No. 1.3e-13;
tive 0; Mismatches 190; Indels
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52.8%; Pred. No. 6.5e-12;
tive 0; Mismatches 194; Indels
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Patent No. 6387680
                                                            Best Local Similarity 53.8 Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 224; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 ACGA 611
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US-09-820-001-1
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US-09-186-489-4
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Length 1137; Indels

236

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TICCTITIAICTCTTCAGCATAICCCACATGGCAAAAATAAAGCAGCAGATA---GTACT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 AATGTCCGTGGAACGCGTTGCAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 TICIGGGATIGGAGCIGGCAAGAGITAGCIGAAIAIGACCITITAGCAAIGCIAGGCI-- 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 -ATGTGTATACAGTCACACTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATA 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 CAGCTGCTCCTGCCACTCGGCTACCCCTGCACCGAGCACGACGTTGAAACAAAGATGGA 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blanchard, Claire
APPLICANT: Bancourt, Claude
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
APLICANT: O'INVERTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                     0; Mismatches 216;
                                                                                                                         4.3%; Score 64.4; DB 2; 49.8%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JMBER: US/08/227,108
03-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08227108
Patent No. 5807726
GENERAL INFORMATION:
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IBM PC compatible
  MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                            1..1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
: U.S.A.
                                                                                                                                               Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03 CLASSIFICATION:
                                         CDS
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ZIP: 10036
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                                           NAME/KEY:
                                                                 LOCATION:
                                                                                  US-09-073-674-2
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                                                                                                                             Query Match
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CTGCCCAACAACAGCCTGGCCTTCATCCTGGCCGACGCCGGGTACGACGTGTGGCTGGGG 291
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                                                                                TTCCTTTTATCTTTCAGCATATCCCACATGGCAAAAATAAAGCAGCAGAAAA---GTACT
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APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: Warner-Lambert Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/073,674
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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NAME: CTISSEY, TOOM M.
REGISTRATION NUMBER: 5072
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEPHONE: 734 622-1553
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LENGTH: 1137 base pairs
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INFORMATION FOR SEQ ID NO:
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EDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2800 Plyr
CITY: Ann Arbor
STATE: Michigan
COUNTRY: U.S.A.
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TOPOLOGY: lin
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US-09-073-674-4
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Best Local Similarity 49.8%; Pred. No. 1.9e-07;
Matches 220; Conservative 0; Mismatches 216; Indels
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Patent No. 5998189
GENERAL INFORMATION
APPLICANT: Blanchard, Claire
APPLICANT: Blanchard, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INFORTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Warner-Lambert Company
STREET: 2800 Plymouth Road
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS;
LENGTH: 1140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA tO mRNA
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STATE: Michigan
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; LOCATION: 1...
US-08-227-108-4
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US-09-073-674-4
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176 CAGCTGCTCCTGCCACTCGGCTACCCCTGCACCGAGCACGTTGAAACAAAAGATGGA 235
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APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 64.4; DB 2;
49.8%; Pred. No. 1.9e-07;
live 0; Mismatches 216;
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072-D1-66-TMC
TELECOMMUNICATION INFORMATION:
TELEFHONE: 734 622-7530
                                                                           US/09/073,674
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Patent No. 5807726
GENERAL INFORMATION:
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Best Local Similarity 49.8'
Matches 220; Conservative
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                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STRANDEDNESS: double
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Pred. No. 1.9e-07;
0; Mismatches 216; Indels 6
                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03.4PR-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/POCKET NUMBER: 7620-033
TELEPHONE: 212 790-9090
TELEPHONE: 212 869-8864/9741
TELEX: 212 869-8864/9741
TELEX: 212 869-8864/9741
SELEX: 1116 PENNIE
SEQUENCE CHARACTERISTICS:
                               the Americas
                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         590 ATGGGTTTGGCGGCTTTGACGA 611
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              E: Pennie & Edmonds
1155 Avenue of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: CDNA to mRNA US-08-227-108-6
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1146 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.3
Best Local Similarity 49.8
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                             New York
New York
XY: U.S.A.
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                                                             STATE: N
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US-09-073-674-6
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172 AGACCTGTTGCATTTTTGCAACAGGTTTGCTCGCATCAGCCACAAAACTGGATCTCCAAC 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCTGGGATTGGAGCTGGCAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCT-- 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 -ATGTGTATACAGTCACACAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATA 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 CAGATGATCACCTACTGGGGATACCCAGCTGAGGAATATGAAGTTGTGACCGAAGACGGT 111
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                                                                                                                      Recombinant Dog Gastric Lipase
                                                                                                                                                                                                                                                                                                                                                       TBM PC compartible
SYERM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%; Score 64.4; DB 2;
49.8%; Pred. No. 1.9e-07;
tive 0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5072-D1-66-TMC
                                                                                                                                                                                            Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/073,674 FILING DATE:
                                                                                              APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinat
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AMME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
                                                                                                                                                                                       ADDRESSEE: Warner-Lambert (
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: Michigan
                                                  Blanchard, Claire
Benicourt, Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: CDNA to mRNA US-09-073-674-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1146 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.3'
Best Local Similarity 49.8'
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                        U.S.A.
Patent No. 5998189
GENERAL INFORMATION:
APPLICANT: Blanch
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                                                                                                                                                                                                                                                                                                           48105
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
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                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                   COUNTRY:
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590 ATGGGTTTGGCGGCTTTGACGA 611

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Sequence 6, Application US/09073674

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353 TCTGCTGAGCAATCACTTGGGGTATATCCTTGCTGATAACGGTTTTGATGTTTTGGATTGGG 412
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                                           531 -ATGTGTATACAGTCACACAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAACTATA 589
                                                               176 CAGCTGCTCCTGCCACTCGGCTACCCCTGCACCGAGCACAACGTTGAAACAAAGATGGA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 CAGATGATCACCTACTGGGGATACCCAGCTGAGGAATATGAAGTTGTGACCGAAGACGGT 111
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
CORRESPONDENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64.4; DB 2;
Pred. No. 2.2e-07;
0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5072-D1-66-TMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warner-Lambert Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: CISSEN, TOOM M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEPHONE: 734 622-1553
                                                                                                                                                                                                                                                           US-09-073-674-1; Sequence I. Application US/09073674; Sequence I. Application US/09073674; Patent No. 5998189; GENERAL INPORMATION:
                                                                                                                                                    590 ATGGGTTTGGCGGCTTTGACGA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: CDNA to mRNA US-09-073-674-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1528 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 49.8
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 CAGATGATCACCTACTGGGGATACCCAGCTGAGGAATATGAAGTTGTGACCGAAGACGGT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3%; Score 64.4; DB 1; Length 1:
49.8%; Pred. No. 2.2e-07;
iive 0; Mismatches 216; Indels
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
APPLICANT: Arnien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Alian A.
RECISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033
TELECHOME: 212 790-9090
TELECHOME: 212 790-9090
TELECHAX: 512 869-8864/971
TELEFAX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1252 Base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           Sequence 1, Application US/08227108
Patent No. 5807726
472 ATTGGTTTCATCGCCTTTTCCA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
US-08-227-108-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 49.8
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                      CITY: Nev
STATE: Ne
COUNTRY:
                                                                                                    US-08-227-108-1
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TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001186
CURRENT APPLICATION NUMBER: US/09/820,001
CURRENT APPLICATION NUMBER: 2001-03-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 TAAACTCTGCTGAGCAATCACTTGGGTATATCCTTGCTGATAACGGTTTTGATGTTTGGA 407
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413 AATGTCCGTGGAACGCGTTGGAGTAAAGGTCATTCAACCTTTTCTGTTCATGATAAGCTT 472
                             292 AACAGCAGGGCAACACCTGGGCCAGGAGGAATCTGTACTACTCGCCCGACTCCGTCGAA 351
                                                                                               288 GTACTGGCCCTCCAGTTTTTCTTCAACATGGTCTTTTTCAGGGAGAGACACATGGTTCA 347
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Patent No. 6417002

GENERAL INFORMATION:

APPLICANT: HOTLICK, Robert

TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES

FILE REFERENCE: 0867/00905;

CURRENT APPLICATION NUMBER: US/09/249,585A

CURRENT FILING DATE: 1999-02-11

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO 4
                                                                           TTCTGGGATTGGAGCTGGCAAGAGTTAGCTGAATATGACCTTTTAGCAATGCTAGGCT--
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Pred. No. 0.001;
0; Mismatches 93; Indels
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US-09-820-001-3
; Sequence 3, Application US/09820001
; Patent No. 6387680
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 472 ATTGGTTTCATCGCCTTTTCCA 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.5%;
Best Local Similarity 53.7%;
Matches 108; Conservative
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; ORGANISM: Human
US-09-820-001-3
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LENGTH: 22067
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US-09-249-585A-4
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